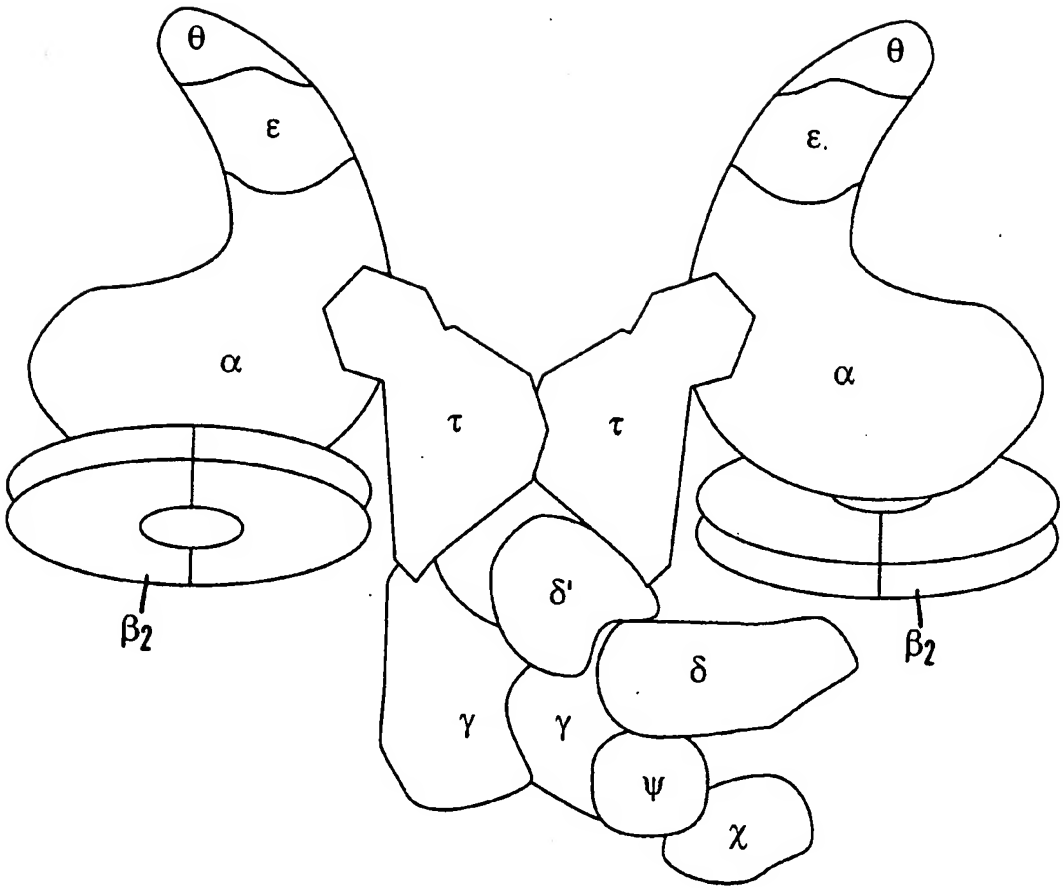

FIG. 1

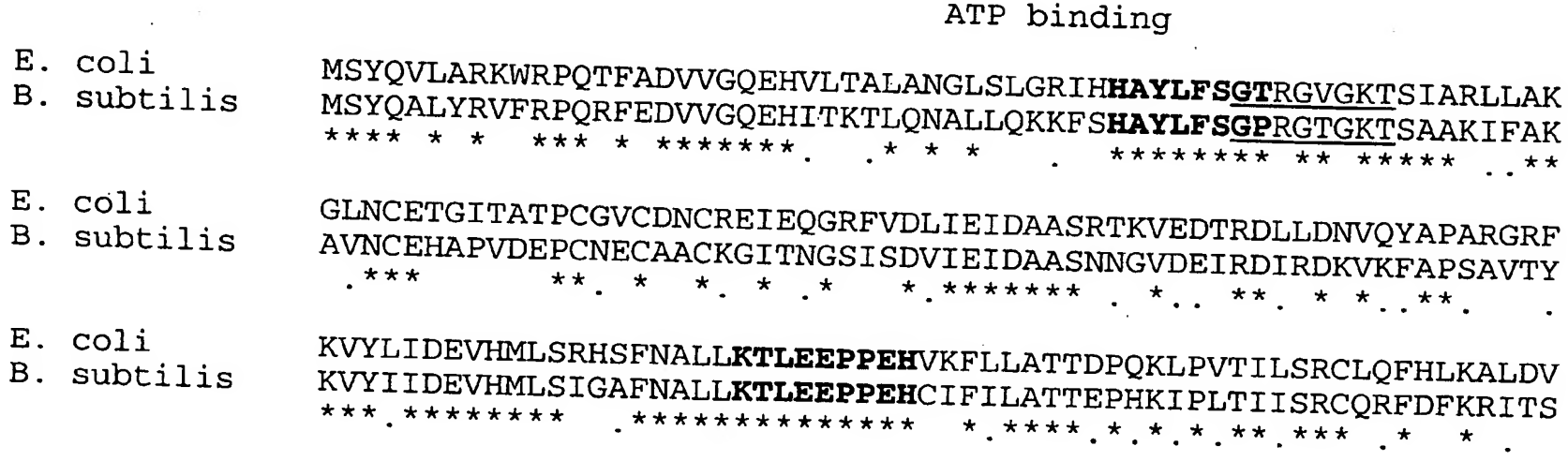

FIG. 2

REPLACEMENT SHEET

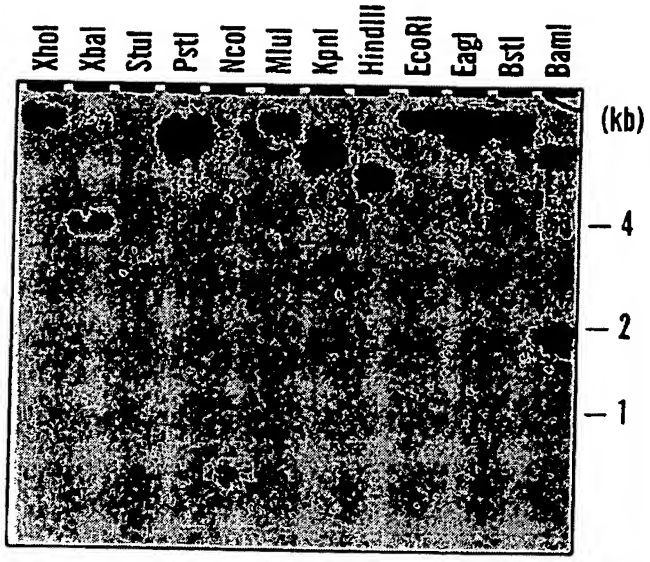
XhoI
XbaI
StuI
PstI
NcoI
MluI
KpnI
HindIII
EcoRI
EagI
BstI
BamI
(kb)
4
2
1

FIG. 3

```
TCCGGGGGTG    GGGTTCCCAG    GTAGACCCCG    GCCCCTCCCG    TGAGCCCCTT    TACCCAGGCC    60

GCCACCTCCT    CCAGGGGGGC    CAAGGCGTGC    AAGGAGAGGA    ACGTCCGCAC    CACGCCCTAT    120
                                                                     S.D.

ACTAGCCTT   GTG AGC GCC CTC TAC CGC CGC TTC CGC CCC CTC ACC TTC CAG GAG GTG GTG    180
            met ser ala leu tyr arg arg phe arg pro leu thr phe gln glu val val    (17)

                                                                          CAC
GGG CAG GAG CAC GTG AAG GAG CCC CTC CTC AAG GCC ATC CGG GAG GGG AGG CTC GCC CAG    240
gly gln glu his val lys glu pro leu leu lys ala ile arg glu gly arg leu ala gln    (37)

GCS TAC CTS TTC TCC GGS AC
GCC TAC CTC TTC TCC GGG CCC AGG GGC GTG GGC AAG ACC ACC ACG GCG AGG CTC CTC GCC    300
ala tyr leu phe ser gly pro arg gly val gly lys thr thr thr ala arg leu leu ala    (57)

ATG GCG GTG GGG TGC CAG GGG GAA GAC CCC CCT TGC GGG GTC TGC CCC CAC TGC CAG GCG    360
met ala val gly cys gln gly glu asp pro pro cys gly val cys pro his cys gln ala    (77)

GtG CAG AGG GGC GCC CAC CCG GAC GTG GTG GAC ATT GAC GCC GCC AGC AAC AAC TCC GTG    420
val gln arg gly ala his pro asp val val asp ile asp ala ala ser asn asn ser val    (97)

GAG GAC GTG CGG GAG CTG AGG GAA AGG ATC CAC CTC GCC CCC CTC TCT GCC CCC AGG AAG    480
glu asp val arg glu leu arg glu arg ile his leu ala pro leu ser ala pro arg lys    (117)

                                                                          C
GTC TTC ATC CTG GAC GAG GCC CAC ATG CTC TCC AAA AGC GCC TTC AAC GCC CTC CTC AAG    540
val phe ile leu asp Glu ala his met leu ser lys ser ala phe asn ala leu leu lys    (137)
```

FIG. 4A-1

REPLACEMENT SHEET

REPLACEMENT SHEET

```
TGS CTS CTC CTC GGS GGS CTC GTG
ACC CTG GAG GAG CCC CCG CCC CAC GTC CTC TTC GTC TTC GCC ACC ACC GAG CCC GAG AGG   600
thr leu glu glu pro pro pro his val leu phe val phe ala thr thr glu pro glu arg  (157)

ATG CCC CCC ACC ATC CTC TCC CGC ACC CAG CAC TTC CGC TTC CGC CGC CTC ACG GAG GAG   660
met pro pro thr ile leu ser arg thr gln his phe arg phe arg arg leu thr glu glu  (177)

GAG ATC GCC TTT AAG CTC CGG CGC ATC CTG GAG GCC GTG GGG CGG GAG GCG GAG GAG GAG   720
glu ile ala phe lys leu arg arg ile leu glu ala val gly arg glu ala glu glu glu  (197)

GCC CTC CTC CTC CTC GCC CGC CTG GCG GAC GGG GCC CTT AGG GAC GCG GAA AGC CTC CTG   780
ala leu leu leu leu ala arg leu ala asp gly ala leu arg asp ala glu ser leu leu  (217)

GAG CGC TTC CTC CTC CTG GAA GGC CCC CTC ACC CGG AAG GAG GTG GAG CGC GCC CTA GGC   840
glu arg phe leu leu leu glu gly pro leu thr arg lys glu val glu arg ala leu gly  (237)

TCC CCC CCA GGG ACC GGG GTG GCC GAG ATC GCC GCC TCC CTC GCG AGG GGG AAA ACG GCG   900
ser pro pro gly thr gly val ala glu ile ala ala ser leu ala arg gly lys thr ala  (257)

GAG GCC CTG GGC CTC GCC CGG CGC CTC TAC GGG GAA GGG TAC GCC CCG AGG AGC CTG GTC   960
glu ala leu gly leu ala arg arg leu tyr gly glu gly tyr ala pro arg ser leu val  (277)

TCG GGC CTT TTG GAG GTG TTC CGG GAA GGC CTC TAC GCC GCC TTC GGC CTC GCG GGA ACC  1020
ser gly leu leu glu val phe arg glu gly leu tyr ala ala phe gly leu ala gly thr  (297)

CCC CTT CCC GCC CCG CCC CAG GCC CTG ATC GCC GCC ATG ACC GCC CTG GAC GAG GCC ATG  1080
pro leu pro ala pro pro gln ala leu ile ala ala met thr ala leu asp glu ala met  (317)
```

FIG. 4A-2

```
GAG CGC CTC GCC CGC CGC TCC GAC GCC TTA AGC CTG GAG GTG GCC CTC CTG GAG GCG GGA  1140
glu arg leu ala arg arg ser asp ala leu ser leu glu val ala leu leu glu ala gly  (337)

AGG GCC CTG GCC GCC GAG GCC CTA CCC CAG CCC ACG GGC GCT CCT TCC CCA GAG GTC GGC  1200
arg ala leu ala ala glu ala leu pro gln pro thr gly ala pro ser pro glu val gly  (357)

CCC AAG CCG GAA AGC CCC CCG ACC CCG GAA CCC CCA AGG CCC GAG GAG GCG CCC GAC CTG  1260
pro lys pro glu ser pro pro thr pro glu pro pro arg pro glu glu ala pro asp leu  (377)

CGG GAG CGG TGG CGG GCC TTC CTC GAG GCC CTC AGG CCC ACC CTA CGG GCC TTC GTG CGG  1320
arg glu arg trp arg ala phe leu glu ala leu arg pro thr leu arg ala phe val arg  (397)

GAG GCC CGC CCG GAG GTC CGG GAA GGC CAG CTC TGC CTC GCT TTC CCC GAG GAC AAG GCC  1380
glu ala arg pro glu val arg glu gly gln leu cys leu ala phe pro glu asp lys ala  (417)

TTC CAC TAC CGC AAG GCC TCG GAA CAG AAG GTG AGG CTC CTC CCC CTG GCC CAG GCC CAT  1440
phe his tyr arg lys ala ser glu gln lys val arg leu leu pro leu ala gln ala his  (437)

                                        frameshift site
TTC GGG GTG GAG GAG GTC GTC CTC GTC CTG GAG GGA GAA AAA AAA AGC CTG AGC CCA AGG  1500
phe gly val glu glu val val leu val leu glu gly glu lys lys ser leu ser pro arg  (457)
```

FIG. 4B-1

REPLACEMENT SHEET

```
CCC CGC CCG GCC CCA CCT CCT GAA GCG CCC GCA CCC CCG GGC CCT CCC GAG GAG GAG GTA  1560
pro arg pro ala pro pro pro glu ala pro ala pro pro gly pro pro glu glu glu val  (477)

GAG GCG GAG GAA GCG GCG GAG GAG GCC CCG GAG GAG GCC TTG AGG CGG GTG GTC CGC CTC  1620
glu ala glu glu ala ala glu glu ala pro glu glu ala leu arg arg val val arg leu  (497)

CTG GGG GGG CGG GTG CTC TGG GTG CGG CGG CCC AGG ACC CGG GAG GCG CCG GAG GAG GAA  1680
leu gly gly arg val leu trp val arg arg pro arg thr arg glu ala pro glu glu glu  (517)

CCC CTG AGC CAA GAC GAG ATA GGG GGT ACT GGT ATA TAA    TGGGGGCATG   ACGCGGACCAC  1740
pro leu ser gln asp glu ile gly gly thr gly ile *                                 (529)

CGACCTCGGA   CAAGAGACCG   TGGACAACAT   CCTCAAGCGC   CTCCGCCGTA   TTGAGGGCCA  1820

GGTGCGGGGG   CTCCAGAAGA   TGGTGGCCGA   GGGCCGCCCC   TGCGACGAGG   TCCTCACCCA  1880

GATGACCGCC   ACCAAGAAGG   CCATGGAGGC   GGCGGCCACC   CTGATCCTCC   ACGAGTTCCT  1940

GAACGTCTGC   GCCGCCGAGG   TCTCCGAGGG   CAAGGTGAAC   CCCAAGAAGC   CCGAGGAGAT  2000

CGCCACCATG   CTGAAGAACT   TCATCTA                                            2027
```

FIG. 4B-2

REPLACEMENT SHEET

GTG AGC GCC CTC TAC CGC CGC TTC CGC CCC CTC ACC TTC CAG GAG GTG GTG 51
GGG CAG GAG CAC GTG AAG GAG CCC CTC CTC AAG GCC ATC CGG GAG GGG AGG CTC GCC CAG 111
GCC TAC CTC TTC TCC GGG CCC AGG GGC GTG GGC AAG ACC ACC ACG GCG AGG CTC CTC GCC 171
ATG GCG GTG GGG TGC CAG GGG GAA GAC CCC CCT TGC GGG GTC TGC CCC CAC TGC CAG GCG 231
GtG CAG AGG GGC GCC CAC CCG GAC GTG GTG GAC ATT GAC GCC GCC AGC AAC AAC TCC GTG 291
GAG GAC GTG CGG GAG CTG AGG GAA AGG ATC CAC CTC GCC CCC CTC TCT GCC CCC AGG AAG 351
GTC TTC ATC CTG GAC GAG GCC CAC ATG CTC TCC AAA AGC GCC TTC AAC GCC CTC CTC AAG 411
ACC CTG GAG GAG CCC CCG CCC CAC GTC CTC TTC GTC TTC GCC ACC ACC GAG CCC GAG AGG 471
ATG CCC CCC ACC ATC CTC TCC CGC ACC CAG CAC TTC CGC TTC CGC CGC CTC ACG GAG GAG 531
GAG ATC GCC TTT AAG CTC CGG CGC ATC CTG GAG GCC GTG GGG CGG GAG GCG GAG GAG GAG 591
GCC CTC CTC CTC CTC GCC CGC CTG GCG GAC GGG GCC CTT AGG GAC GCG GAA AGC CTC CTG 651
GAG CGC TTC CTC CTC CTG GAA GGC CCC CTC ACC CGG AAG GAG GTG GAG CGC GCC CTA GGC 711
TCC CCC CCA GGG ACC GGG GTG GCC GAG ATC GCC GCC TCC CTC GCG AGG GGG AAA ACG GCG 771
GAG GCC CTG GGC CTC GCC CGG CGC CTC TAC GGG GAA GGG TAC GCC CCG AGG AGC CTG GTC 831
TCG GGC CTT TTG GAG GTG TTC CGG GAA GGC CTC TAC GCC GCC TTC GGC CTC GCG GGA ACC 891
CCC CTT CCC GCC CCG CCC CAG GCC CTG ATC GCC GCC ATG ACC GCC CTG GAC GAG GCC ATG 951
GAG CGC CTC GCC CGC CGC TCC GAC GCC TTA AGC CTG GAG GTG GCC CTC CTG GAG GCG GGA 1011
AGG GCC CTG GCC GCC GAG GCC CTA CCC CAG CCC ACG GGC GCT CCT TCC CCA GAG GTC GGC 1071
CCC AAG CCG GAA AGC CCC CCG ACC CCG GAA CCC CCA AGG CCC GAG GAG GCG CCC GAC CTG 1131
CGG GAG CGG TGG CGG GCC TTC CTC GAG GCC CTC AGG CCC ACC CTA CGG GCC TTC GTG CGG 1191
GAG GCC CGC CCG GAG GTC CGG GAA GGC CAG CTC TGC CTC GCT TTC CCC GAG GAC AAG GCC 1251
TTC CAC TAC CGC AAG GCC TCG GAA CAG AAG GTG AGG CTC CTC CCC CTG GCC CAG GCC CAT 1311
TTC GGG GTG GAG GAG GTC GTC CTC GTC CTG GAG GGA GAA AAA AAA AGC CTG AGC CCA AGG 1371
CCC CGC CCG GCC CCA CCT CCT GAA GCG CCC GCA CCC CCG GGC CCT CCC GAG GAG GAG GTA 1431
GAG GCG GAG GAA GCG GCG GAG GAG GCC CCG GAG GAG GCC TTG AGG CGG GTG GTC CGC CTC 1491
CTG GGG GGG CGG GTG CTC TGG GTG CGG CGG CCC AGG ACC CGG GAG GCG CCG GAG GAG GAA 1551
CCC CTG AGC CAA GAC GAG ATA GGG GGT ACT GGT ATA TAA (1590)

FIG. 4C

Met ser ala leu tyr arg arg phe arg pro leu thr phe gln glu val val gly gln glu 20
his val lys glu pro leu leu lys ala ile arg glu gly arg leu ala gln ala tyr leu 40
phe ser gly pro arg gly val gly lys thr thr thr ala arg leu leu ala met ala val 60
gly cys gln gly glu asp pro pro cys gly val cys pro his cys gln ala val gln arg 80
gly ala his pro asp val val asp ile asp ala ala ser asn asn ser val glu asp val 100
arg glu leu arg glu arg ile his leu ala pro leu ser ala pro arg lys val phe ile 120
leu asp glu ala his met leu ser lys ser ala phe asn ala leu leu lys thr leu glu 140
glu pro pro pro his val leu phe val phe ala thr thr glu pro glu arg met pro pro 160
thr ile leu ser arg thr gln his phe arg phe arg arg leu thr glu glu glu ile ala 180
phe lys leu arg arg ile leu glu ala val gly arg glu ala glu glu glu ala leu leu 200
leu leu ala arg leu ala asp gly ala leu arg asp ala glu ser leu leu glu arg phe 220
leu leu leu glu gly pro leu thr arg lys glu val glu arg ala leu gly ser pro pro 240
gly thr gly val ala glu ile ala ala ser leu ala arg gly lys thr ala glu ala leu 260
gly leu ala arg arg leu tyr gly glu gly tyr ala pro arg ser leu val ser gly leu 280
leu glu val phe arg glu gly leu tyr ala ala phe gly leu ala gly thr pro leu pro 300
ala pro pro gln ala leu ile ala ala met thr ala leu asp glu ala met glu arg leu 320
ala arg arg ser asp ala leu ser leu glu val ala leu leu glu ala gly arg ala leu 340
ala ala glu ala leu pro gln pro thr gly ala pro ser pro glu val gly pro lys pro 360
glu ser pro pro thr pro glu pro pro arg pro glu glu ala pro asp leu arg glu arg 380
trp arg ala phe leu glu ala leu arg pro thr leu arg ala phe val arg glu ala arg 400
pro glu val arg glu gly gln leu cys leu ala phe pro glu asp lys ala phe his tyr 420
arg lys ala ser glu gln lys val arg leu leu pro leu ala gln ala his phe gly val 440
glu glu val val leu val leu glu gly glu lys lys ser leu ser pro arg pro arg pro 460
ala pro pro pro glu ala pro ala pro pro gly pro pro glu glu glu val glu ala glu 480
glu ala ala glu glu ala pro glu glu ala leu arg arg val val arg leu leu gly gly 500
arg val leu trp val arg arg pro arg thr arg glu ala pro glu glu glu pro leu ser 520
gln asp glu ile gly gly thr gly ile 529

FIG. 4D

REPLACEMENT SHEET

9/83

Met ser ala leu tyr arg arg phe arg pro leu thr phe gln glu val val gly gln glu 20
his val lys glu pro leu leu lys ala ile arg glu gly arg leu ala gln ala tyr leu 40
phe ser gly pro arg gly val gly lys thr thr thr ala arg leu leu ala met ala val 60
gly cys gln gly glu asp pro pro cys gly val cys pro his cys gln ala val gln arg 80
gly ala his pro asp val val asp ile asp ala ala ser asn asn ser val glu asp val 100
arg glu leu arg glu arg ile his leu ala pro leu ser ala pro arg lys val phe ile 120
leu asp glu ala his met leu ser lys ser ala phe asn ala leu leu lys thr leu glu 140
glu pro pro pro his val leu phe val phe ala thr thr glu pro glu arg met pro pro 160
thr ile leu ser arg thr gln his phe arg phe arg arg leu thr glu glu glu ile ala 180
phe lys leu arg arg ile leu glu ala val gly arg glu ala glu glu glu ala leu leu 200
leu leu ala arg leu ala asp gly ala leu arg asp ala glu ser leu leu glu arg phe 220
leu leu leu glu gly pro leu thr arg lys glu val glu arg ala leu gly ser pro pro 240
gly thr gly val ala glu ile ala ala ser leu ala arg gly lys thr ala glu ala leu 260
gly leu ala arg arg leu tyr gly glu gly tyr ala pro arg ser leu val ser gly leu 280
leu glu val phe arg glu gly leu tyr ala ala phe gly leu ala gly thr pro leu pro 300
ala pro pro gln ala leu ile ala ala met thr ala leu asp glu ala met glu arg leu 320
ala arg arg ser asp ala leu ser leu glu val ala leu leu glu ala gly arg ala leu 340
ala ala glu ala leu pro gln pro thr gly ala pro ser pro glu val gly pro lys pro 360
glu ser pro pro thr pro glu pro pro arg pro glu glu ala pro asp leu arg glu arg 380
trp arg ala phe leu glu ala leu arg pro thr leu arg ala phe val arg glu ala arg 400
pro glu val arg glu gly gln leu cys leu ala phe pro glu asp lys ala phe his tyr 420
arg lys ala ser glu gln lys val arg leu leu pro leu ala gln ala his phe gly val 440
glu glu val val leu val leu glu gly glu lys lys lys pro asp pro lys ala pro pro 460
gly pro thr ser 464

FIG. 4E

REPLACEMENT SHEET

10/83

```
Met ser ala leu tyr arg arg phe arg pro leu thr phe gln glu val val gly gln glu  20
his val lys glu pro leu leu lys ala ile arg glu gly arg leu ala gln ala tyr leu  40
phe ser gly pro arg gly val gly lys thr thr ala arg leu leu ala met ala val  60
gly cys gln gly glu asp pro pro cys gly val cys pro his cys gln ala val gln arg  80
gly ala his pro asp val val asp ile asp ala ala ser asn asn ser val glu asp val 100
arg glu leu arg glu arg ile his leu ala pro leu ser ala pro arg lys val phe ile 120
leu asp glu ala his met leu ser lys ser ala phe asn ala leu leu lys thr leu glu 140
glu pro pro pro his val leu phe val phe ala thr thr glu pro glu arg met pro pro 160
thr ile leu ser arg thr gln his phe arg phe arg arg leu thr glu glu glu ile ala 180
phe lys leu arg arg ile leu glu ala val gly arg glu ala glu glu ala leu leu leu 200
leu leu ala arg leu ala asp gly ala leu arg asp ala glu ser leu leu glu arg phe 220
leu leu leu glu gly pro leu thr arg lys glu val glu arg ala leu gly ser pro pro 240
gly thr gly val ala glu ile ala ala ser leu ala arg gly lys thr ala glu ala leu 260
gly leu ala arg arg leu tyr gly glu gly tyr ala pro arg ser leu val ser gly leu 280
leu glu val phe arg glu gly leu tyr ala ala phe gly leu ala gly thr pro leu pro 300
ala pro pro gln ala leu ile ala ala met thr ala leu asp glu ala met glu arg leu 320
ala arg arg ser asp ala leu ser leu glu val ala leu leu glu ala gly arg ala leu 340
ala ala glu ala leu pro gln pro thr gly ala pro ser pro glu val gly pro lys pro 360
glu ser pro pro thr pro glu pro pro arg pro glu glu ala pro asp leu arg glu arg 380
trp arg ala phe leu glu ala leu arg pro thr leu arg ala phe val arg glu ala arg 400
pro glu val arg glu gly gly gln leu cys leu ala phe pro glu asp lys ala phe his tyr 420
arg lys ala ser glu gln lys val arg leu leu pro leu ala gln ala his phe gly val 440
glu glu val val leu val leu glu gly glu lys lys lys ala                      454
```

FIG. 4F

```
                                                          ATP site
E.coli    MSYQVLARKWRPQTFADVVGQEHVLTALANGLSLGRIHHAYLFSGTRGVGKTSIARLLAK   60
H.inf.    ............K.........II.......KDN.L.....................F..   60
B.sub.    ....A.Y.VF...R.E.......ITKT.Q.A.LQKKFS.......P..T....A.KIF..   60
C.cres.   DA.T.....Y..R..E.LI...AMVRT...AF.T...A..FMLT.V......TT.....R  113
M.gen.    -MH..FYQ.Y..IN.KQTL...SIRKI.V.AINRDKLPNG.I...E..T...TF.KII..   59
T.th.     --VSA.Y.RF..L..QE.......KEP.LKAIRE..LAQ......P......TT.....M   58

                Zn++ finger
          *             *  *  *
E.coli    GLNCET----GITATPCGVCDNCREIEQGRFVDLIEIDAASRTKVEDTRDLLDNVQYAPA  116
H.inf.    ....VH----.V......E.E..KA....N.I.................E.......K.V  116
B.sub.    AV...H----APVDE..NE.AA.KG.TN.SIS.V.......NNG.DEI..IR.K.KF..S  116
C.cres.   A..Y..DTVK.PSVDLTTEGYH..S.IE..HM.VL.L........DEM.E...G.R...V  173
M.gen.    AI..LN----WDQIDV.NS..V.KS.NTNSAI.IV......KNGIN.I.E.VE..FNH.F  115
T.th      AVG.QG------EDP.....PH.QAVQR.AHP.VVD.....NNS...V.E.RERIHL..L  112

E.coli    RGRFKVYLIDEVHMLSRHSFNALLKTLEEPPEHVKFLLATTDPQKLPVTILSRCLQFHLK  176
H.inf.    V.............................Y.............................  176
B.sub.    AVTY...I........IGA..............CI.I....E.H.I.L..I...QR.DF.  176
C.cres.   EA.Y...I........TAA............P.A..IF...EIR.V........QR.D.R  233
M.gen.    TFKK...IL..A...TTQ.WGG.......S.PY.L.IFT..EFN.I.L......QS.FF.  175
T.th.     SAPR..FIL..A....KSA............P..L.VF...E.ERM.P.....TQH.RFR  172
```

FIG. 5A

REPLACEMENT SHEET

12/83

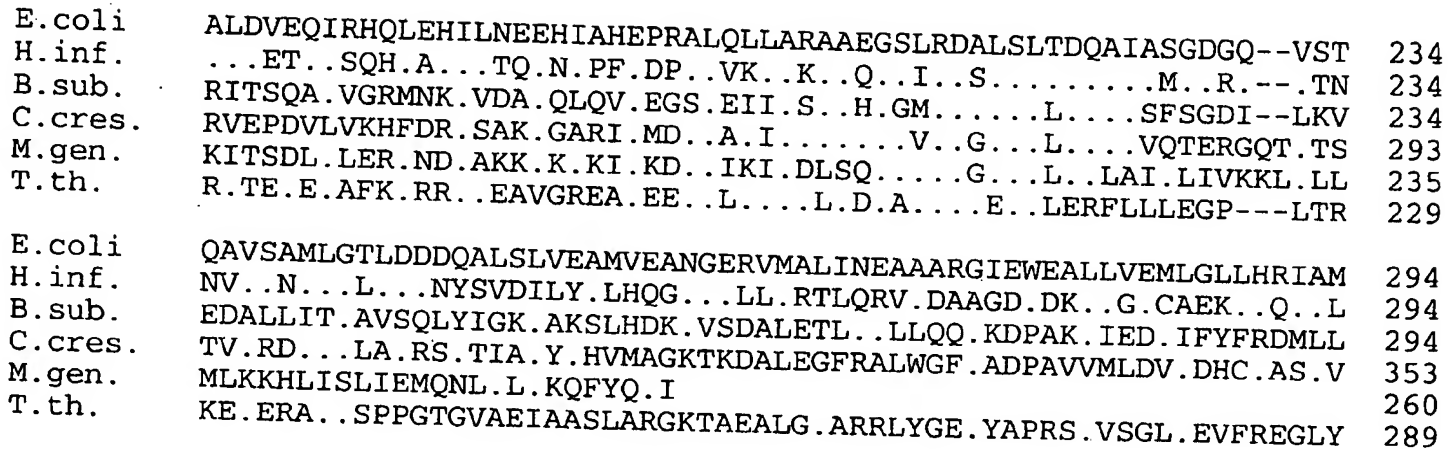

FIG. 5B

REPLACEMENT SHEET

13/83

CC
A C
C C
G-C
C-G
C-G
C-G
G-C
C C
G-C
A-U
C
C
GA
GGAGC
-1 stop
CCACCUCCU
GAUGGAGGA
G-C
C C
C C
C-G
C-G
G-C
G-C
A
A
G
G
C
-2 stop
-2 frame
GUC CUG GAG GGA GAA AAA AAA AGC CUG AGC CCA
val leu glu gly glu lys lys ser leu ser pro
+0 frame

FIG. 6

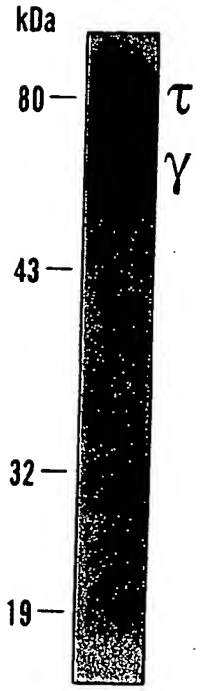

FIG. 7

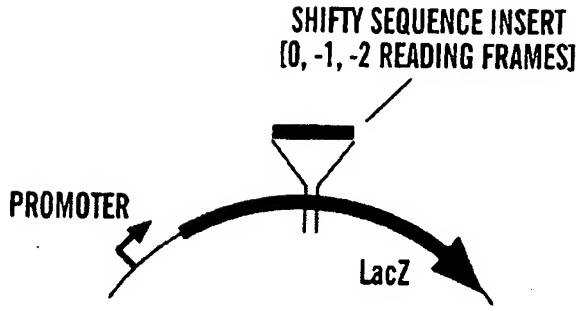

FIG. 8A

	READING FRAME	BLUE	WHITE
SHIFTY SEQUENCE	0	+	
	−1	+	
	−2	+	
MUTANT SEQUENCE	0	++	
	−1		+
	−2		+

FIG. 8B

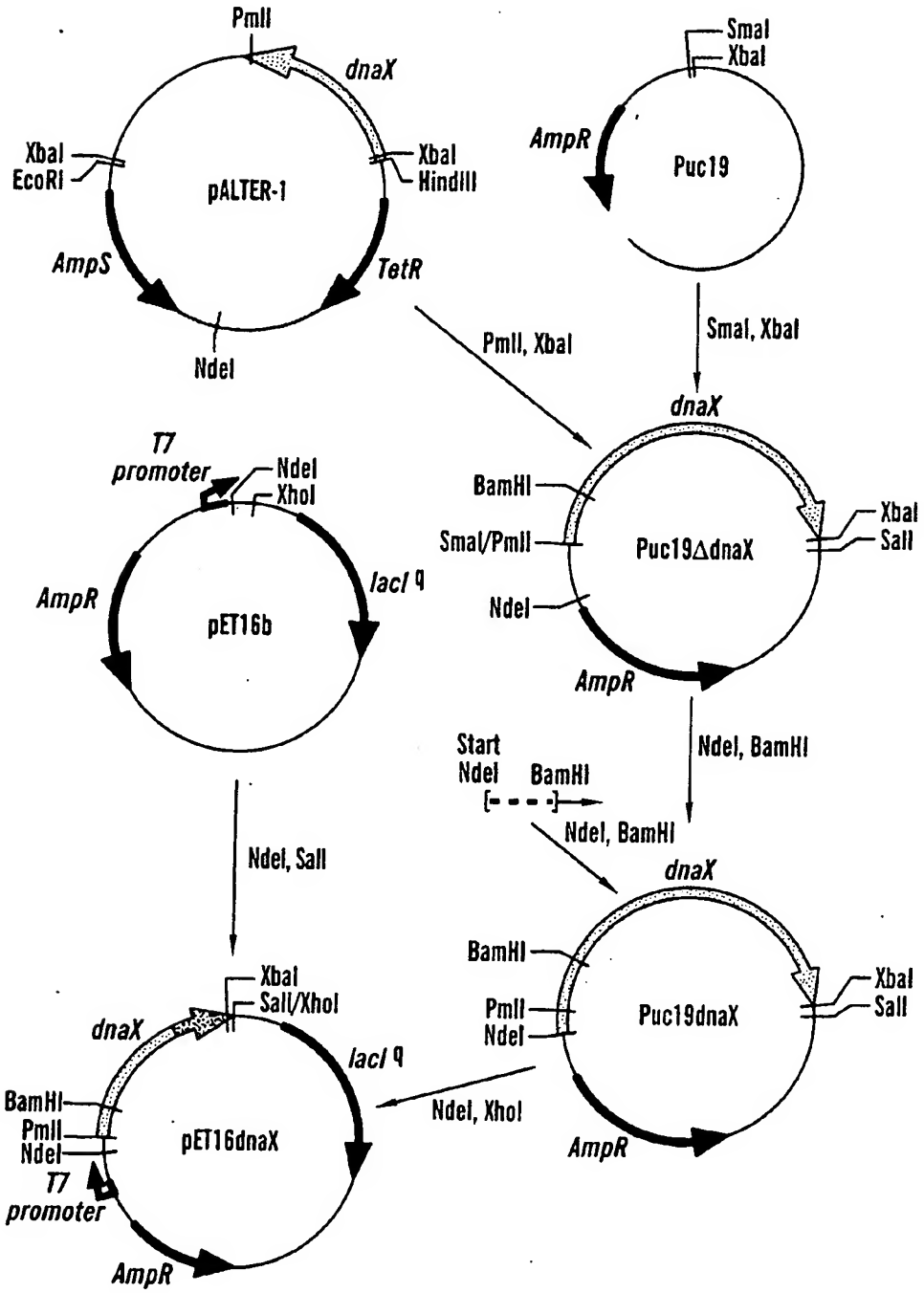
PmlI
dnaX
XbaI
EcoRI
pALTER-1
XbaI
HindIII
AmpS
TetR
NdeI
SmaI
XbaI
AmpR
Puc19
PmlI, XbaI
SmaI, XbaI
dnaX
T7 promoter
NdeI
XhoI
BamHI
SmaI/PmlI
Puc19ΔdnaX
XbaI
SalI
NdeI
AmpR
AmpR
pET16b
lacI q
Start
NdeI
BamHI
NdeI, BamHI
NdeI, BamHI
NdeI, SalI
dnaX
BamHI
PmlI
NdeI
Puc19dnaX
XbaI
SalI
XbaI
SalI/XhoI
dnaX
lacI q
BamHI
PmlI
NdeI
T7 promoter
pET16dnaX
NdeI, XhoI
AmpR
AmpR

FIG. 9

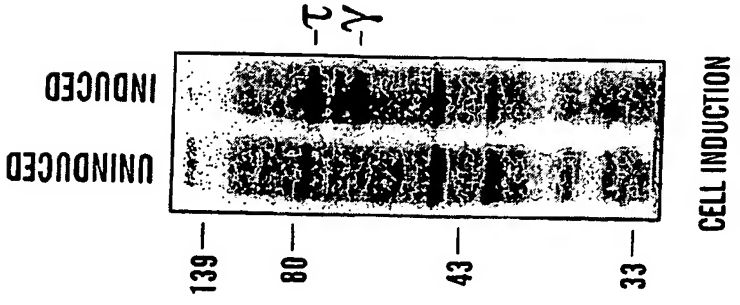

FIG. 10A

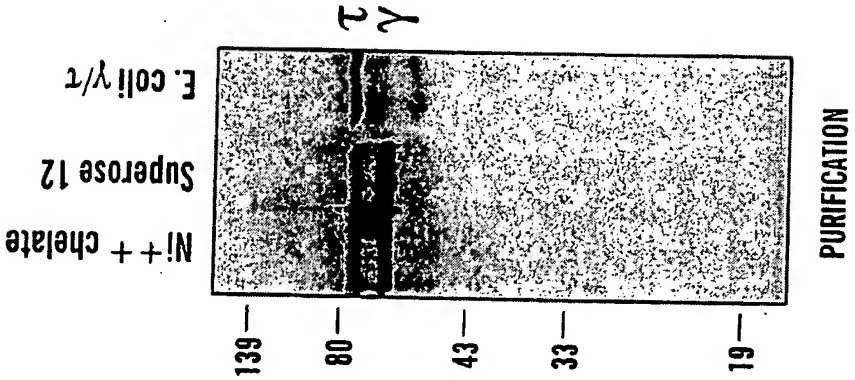

FIG. 10B

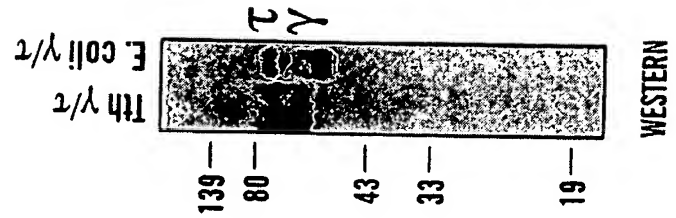

FIG. 10C

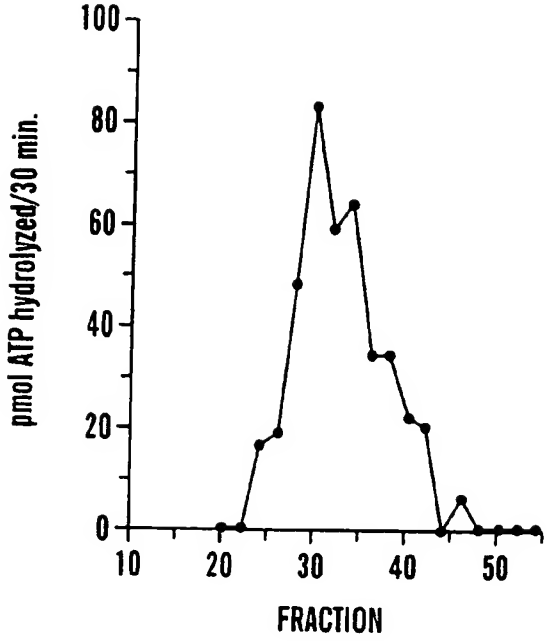

FIG. 11A

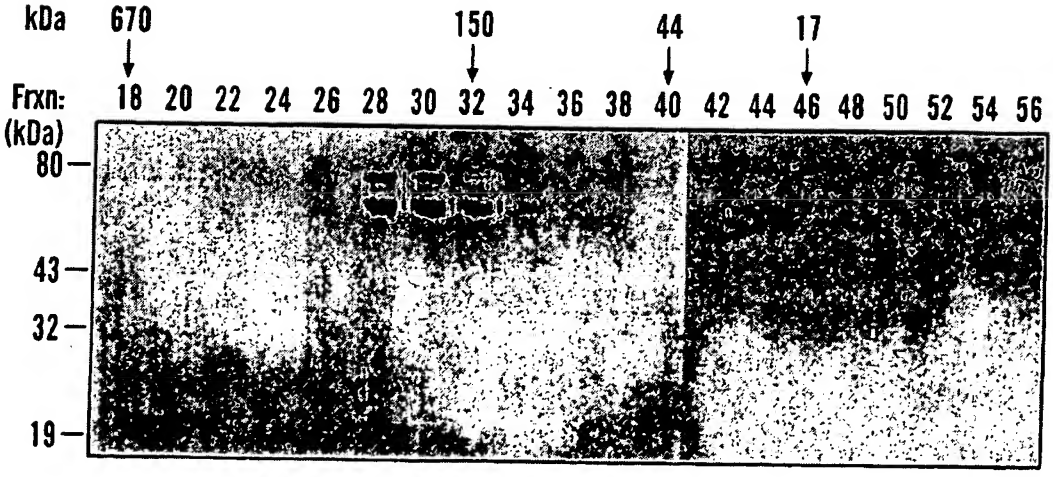

FIG. 11B

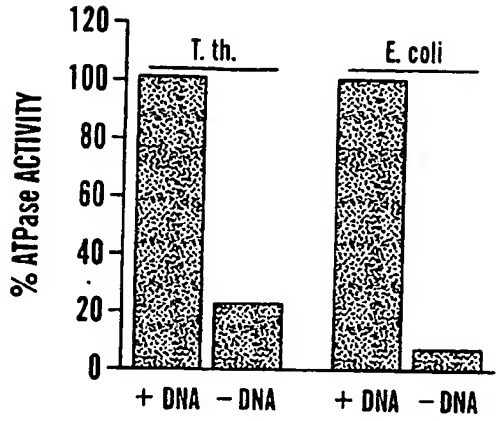

FIG. 12A

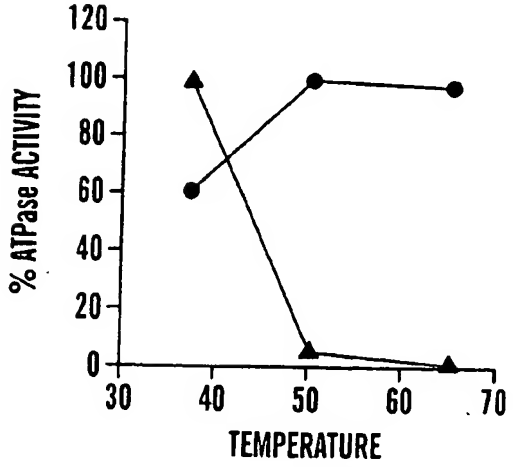

FIG. 12B

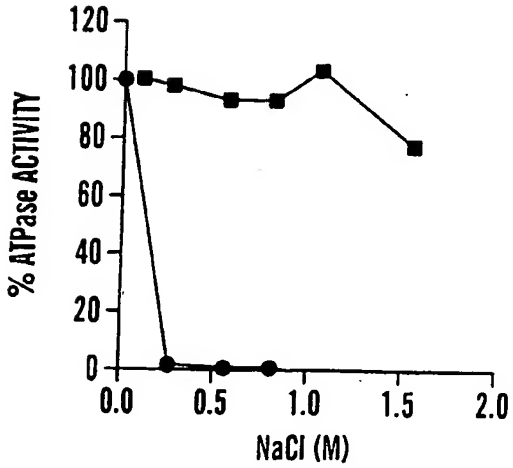

FIG. 12C

FIG. 13A

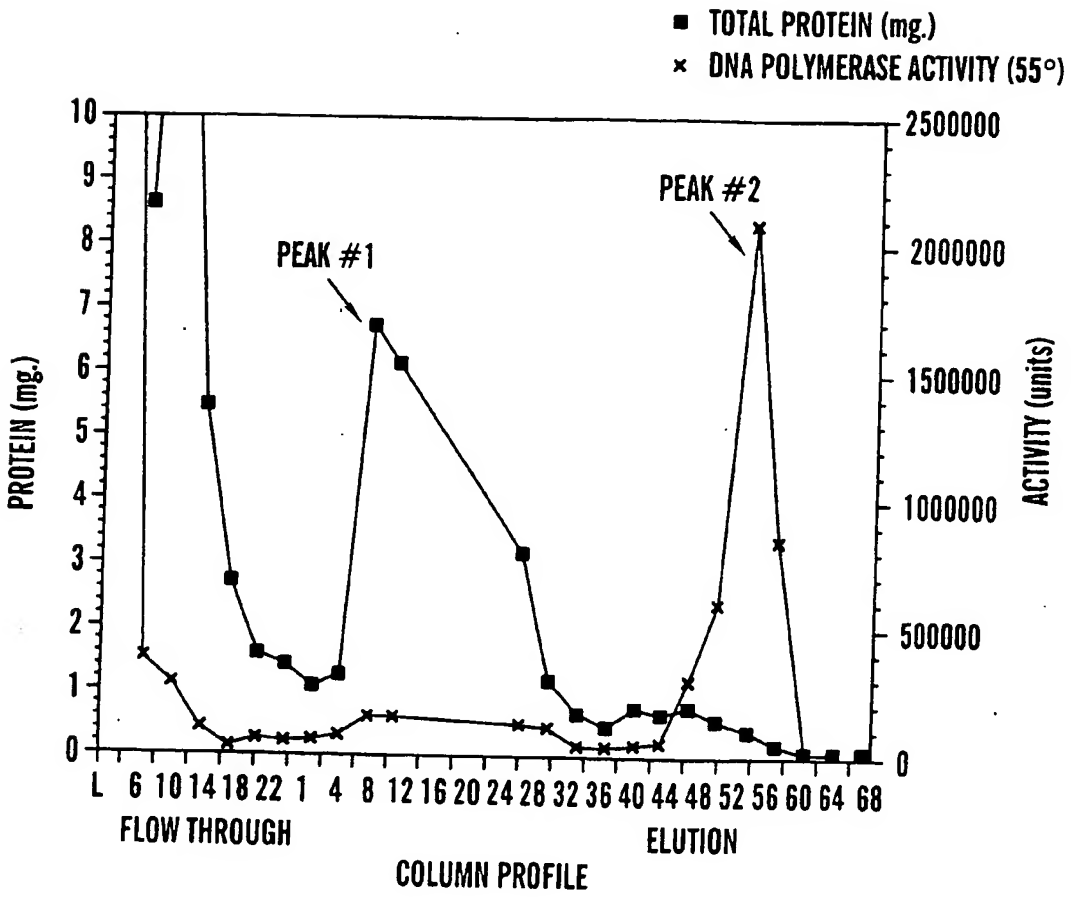

FIG. 13B

ATP AGAROSE STEP COLUMN

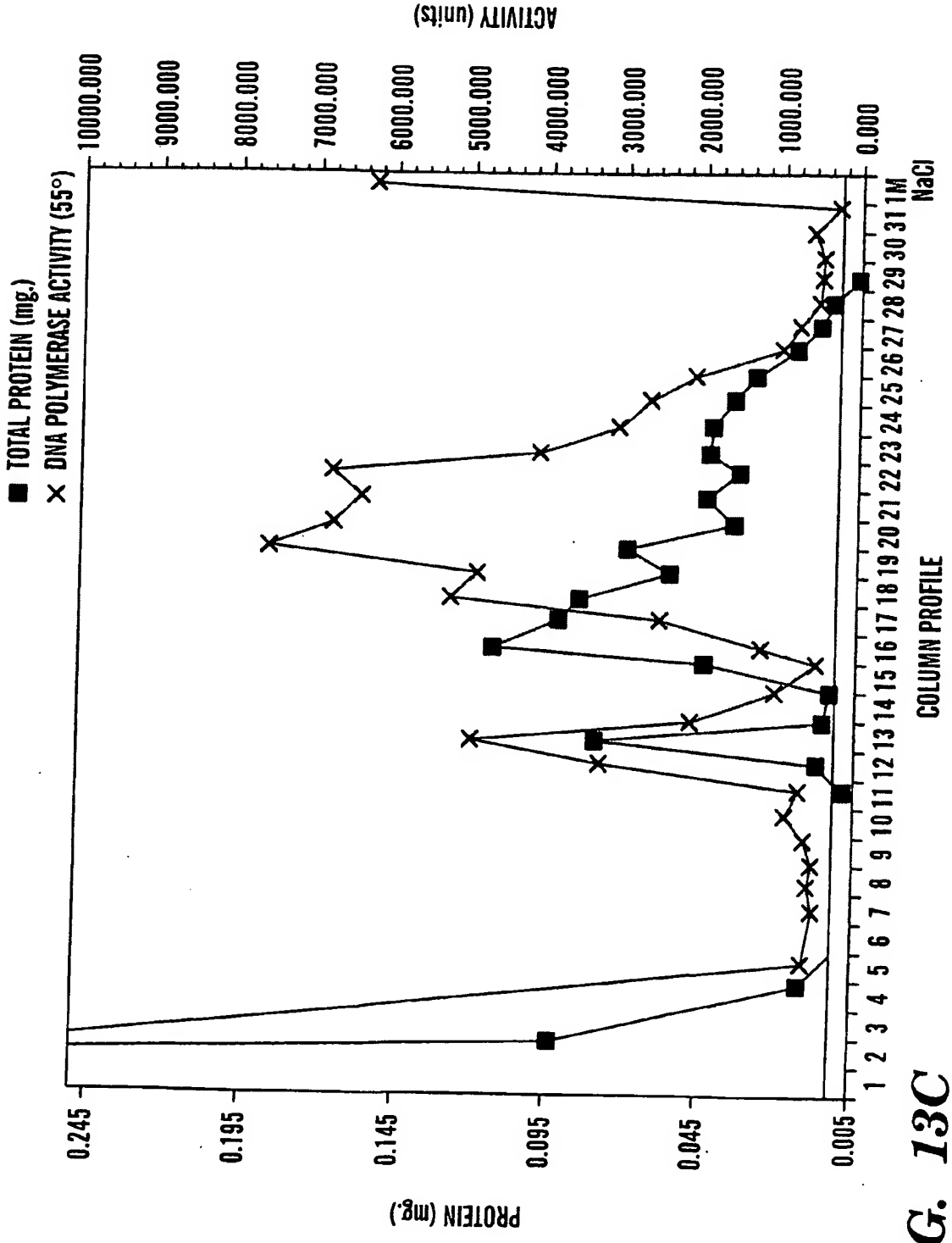
TOTAL PROTEIN (mg.)
DNA POLYMERASE ACTIVITY (55°)
ACTIVITY (units)
PROTEIN (mg.)
10000.000
9000.000
8000.000
7000.000
6000.000
5000.000
4000.000
3000.000
2000.000
1000.000
0.000
0.245
0.195
0.145
0.095
0.045
0.005
1 2 3 4 5 6 7 8 9 10 11 12 13 14 15 16 17 18 19 20 21 22 23 24 25 26 27 28 29 30 31 1M
NaCl
COLUMN PROFILE

FIG. 13C

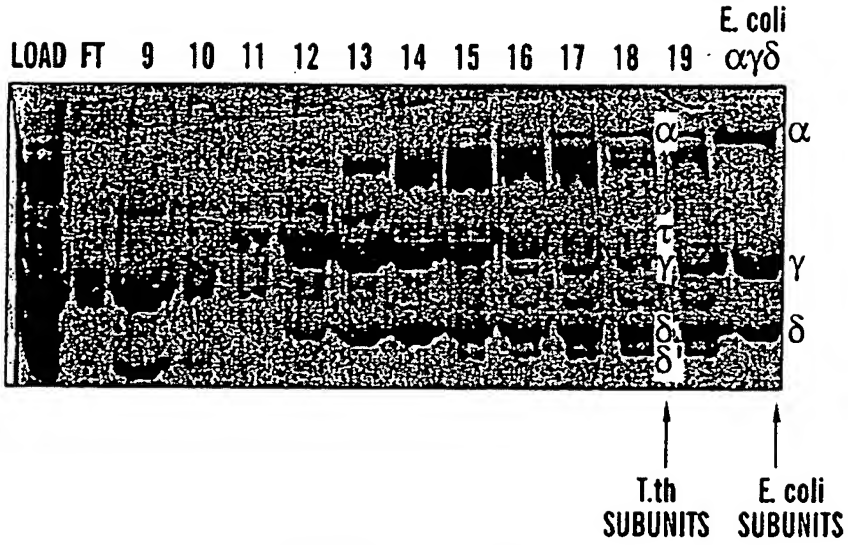

FIG. 14A

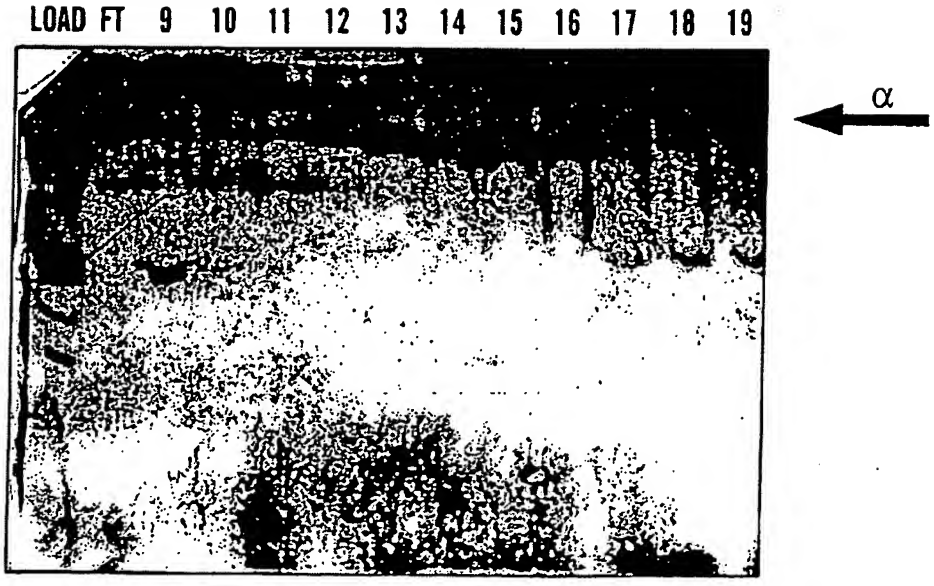

FIG. 14B

Alignment of TTH1 with alphas subunits of other organisms.

```
E.coli      DRYFLELIRTGRPDEESYLHAAVELAEARGLPVV 197   (ID#72)
V.chol.     DHFYLELIRTGRADEESYLHFALDVAEQYDLPVV 197   (ID#73)
H.inf.      DHFYLALSRTGRPNEERYIQAALKLAERCDLPLV 197   (ID#74)
R.prow.     DRFYFEIMRHDLPEEQFIENSYIQIASELSIPIV 195   (ID#75)
H.pyl.      DDFYLEIMRHGILDQRFIDEQVIKMSLETGLKII 213   (ID#76)
S.sp.       DDYYLEIQDHGSVEDRLVNINLVKIAQELDIKIV 202   (ID#77)
M.tub.      DNYFLELMDHGLTIERRVRDGLLEIGRALNIPPL 220   (ID#78)
T.th.         FFIEIQNHGLSEQK                         (ID#61)
```

FIG. 15A

Alignment of TTH2 with alphas subunits of other organisms.

```
E.coli      NKRRAKNGEPPLDIAAIPLDDKKSFDMLQRSETTAVFQLESRGMKD 618 (ID#79)
V.chol.     NPRLKKAGKPPVRIEAIPLDDARSFRNLQDAKTTAVFQLESRGMKE 618 (ID#80)
H.inf.      NVRMVREGKPRVDIAAIPLDDPESFELLKRSETTAVFQLESRGMKD 618 (ID#81)
R.prow.     CKKLLKEQGIKIDFDDMTFDDKKTYQMLCKGKGVGVFQFESIGMKD 624 (ID#82)
H.pyl.      LKIIKTQHKISVDFLSLDMDDPKVYKTIQSGDTVGIFQIES-GMFQ 648 (ID#83)
S.sp.       QERKALQIRARTGSKKLPDDVKKTHKLLEAGDLEGIFQLESQGMKQ 643 (ID#84)
M.tub.      IDNVRANRGIDLDLESVPLDDKATYELLGRGDTLGVFQLDGGPMRD 646 (ID#85)
T.th.               RVELDYDALTLDD                           (ID#60)
```

FIG. 15B

```
ATGGGCCGGGAGCTCCGCTTCGCCCACCTCCACCAGCACA
CCCAGTTCTCCCTCCTGGACGGGGCGGCGAAGCTTTCCGA
CCTCCTCAAGTGGGTCAAGGAGACGACCCCCGAGGACCCC                          120
GCCTTGGCCATGACCGACCACGGCAACCTCTTCGGGGCCG
TGGAGTTCTACAAGAAGGCCACCGAAATGGGCATCAAGCC
CATCCTGGGCTACGAGGCCTACGTGGCGGCGGAAAGCCGC                          240
TTTGACCGCAAGCGGGGAAAGGGCCTAGACGGGGGCTACT
TTCACCTCACCCTCCTCGCCAAGGACTTCACGGGGTACCA
GAACCTGGTGCGCCTGGCGAGCCGGGCTTACCTGGAGGGG                          360
TTTTACGAAAAGCCCCGGATTGACCGGGAGATCCTGCGCG
AGCACGCCGAGGGCCTCATCGCCCTCTCGGGGTGCCTCGG
GGCGGAGATCCCCCAGTTCATCCTCCAGGACCGTCTGGAC                          480
CTGGCCGAGGCCCGGCTCAACGAGTACCTCTCCATCTTCA
AGGACCGCTTCTTCATCGAGATCCAGAACCACGGCCTCCC
CGAGCAGAAAAAGGTCAACGAGGTCCTCAAGGAGTTCGCC                          600
CGAAAGTACGGCCTGGGGATGGTGGCCACCAACGACGGCC
ATTACGTGAGGAAGGAGGACGCCCGCGCCCACGAGGTCCT
CCTCGCCATCCAGTCCAAGAGCACCCTGGACGACCCCGGG                          720
CGCTGGCGCTTCCCCTGCGACGAGTTCTACGTGAAGACCC
CCGAGGAGATGCGGGCCATGTTCCCCGAGGAGGAGTGGGG
GGACGAGCCCTTTGACAACACCGTGGAGATCGCCCGCATG                          840
TGCAACGTGGAGCTGCCCATCGGGGACAAGATGGTCTACC
GAATCCCCCGCTTCCCCCTCCCCGAGGGGCGGACCGAGGC
CCAGTACCTCATGGAGCTCACCTTCAAGGGGCTCCTCCGC                          960
CGCTACCCGGACCGGATCACCGAGGGCTTCTACCGGGAGG
TCTTCCGCCTTTTGGGGAAGCTTCCCCCCCACGGGGACGG
GGAGGCCTTGGCCGAGGCCTTGGCCCAGGTGGAGCGGGAG                         1080
GCTTGGGAGAGGCTCATGAAGAGCCTCCCCCCTTTGGCCG
GGGTCAAGGAGTGGACGGCGGAGGCCATTTTCCACCGGGC
CCTTTACGAGCTTTCCGTGATAGAGCGCATGGGGTTTCCC                         1200
GGCTACTTCCTCATCGTCCAGGACTACATCAACTGGGCCC
GGAGAAACGGCGTCTCCGTGGGGCCCGGCAGGGGGAGCGC
CGCCGGGAGCCTGGTGGCCTACGCCGTGGGGATCACCAAC                         1320
ATTGACCCCCTCCGCTTCGGCCTCCTCTTTGAGCGCTTCC
TGAACCCGGAGAGGGTCTCCATGCCCGACATTGACACGGA
CTTCTCCGACCGGGAGCGGGACCGGGTGATCCAGTACGTG                         1440
CGGGAGCGCTACGGCGAGGACAAGGTGGCCCAGATCGGCA
CCCTGGGAAGCCTCGCCTCCAAGGCCGCCCTCAAGGACGT
GGCCCGGGTCTACGGCATCCCCCACAAGAAGGCGGAGGAA                         1560
TTGGCCAAGCTCATCCCGGTGCAGTTCGGGAAGCCCAAGC
CCCTGCAGGAGGCCATCCAGGTGGTGCCGGAGCTTAGGGC
GGAGATGGAGAAGGACCCCAAGGTGCGGGAGGTCCTCGAG                         1680
GTGGCCATGCGCCTGGAGGGCCTGAACCGCCACGCCTCCG
TCCACGCCGCCGGGGTGGTGATCGCCGCCGAGCCCCTCAC
GGACCTCGTCCCCCTCATGCGCGACCAGGAAGGGCGGCCC                         1800
GTCACCCAGTACGACATGGGGGCGGTGGAGGCCTTGGGGC
TTTTGAAGATGGACTTTTTGGGCCTCCGCACCCTCACCTT
```

FIG. 16A

```
CCTGGACGAGGTCAAGCGCATCGTCAAGGCGTCCCAGGGG                1920
GTGGAGCTGGACTACGATGCCCTCCCCCTGGACGACCCCA
AGACCTTCGCCCTCCTCTCCCGGGGGGAGACCAAGGGGGT
CTTCCAGCTGGAGTCGGGGGGGATGACCGCCACGCTCCGC                2040
GGCCTCAAGCCGCGGCGCTTTGAGGACCTGATCGCCATCC
TCTCCCTCTACCGCCCCGGGCCCATGGAGCACATCCCCAC
CTACATCCGCCGCCACCACGGGCTGGAGCCCGTGAGCTAC                2160
AGCGAGTTTCCCCACGCCGAGAAGTACCTAAAGCCCATCC
TGGACGAGACCTACGGCATCCCCGTCTACCAGGAGCAGAT
CATGCAGATCGCCTCGGCCGTGGCGGGGTACTCCCTGGGC                2280
GAGGCGGACCTCCTGCGGCGGTCCATGGGCAAGAAGAAGG
TGGAGGAGATGAAGTCCCACCGGGAGCGCTTCGTCCAGGG
GGCCAAGGAAAGGGGCGTGCCCGAGGAGGAGGCCAACCGC                2400
CTCTTTGACATGCTGGAGGCCTTCGCCAACTACGGCTTCA
ACAAATCCCACGCTGCCGCCTACAGCCTCCTCTCCTACCA
GACCGCCTACGTGAAGGCCCACTACCCCGTGGAGTTCATG                2520
GCCGCCCTCCTCTCCGTGGAGCGGCACGACTCCGACAAGG
TGGCCGAGTACATCCGCGACGCCCGGGCCATGGGCATAGA
GGTCCTTCCCCCGGACGTCAACCGCTCCGGGTTTGACTTC                2640
CTGGTCCAGGGCCGGCAGATCCTTTTCGGCCTCTCCGCGG
TGAAGAACGTGGGCGAGGCGGCGGCGGAGGCCATTCTCCG
GGAGCGGGAGCGGGGCGGCCCCTACCGGAGCCTCGGCGAC                2760
TTCCTCAAGCGGCTGGACGAGAAGGTGCTCAACAAGCGGA
CCCTGGAGTCCCTCATCAAGGCGGGCGCCCTGGACGGCTT
CGGGGAAAGGGCGCGGCTCCTCGCCTCCCTGGAAGGGCTC                2880
CTCAAGTGGGCGGCCGAGAACCGGGAGAAGGCCCGCTCGG
GCATGATGGGCCTCTTCAGCGAAGTGGAGGAGCCGCCTTT
GGCCGAGGCCGCCCCCCTGGACGAGATCACCCGGCTCCGC                3000
TACGAGAAGGAGGCCCTGGGGATCTACGTCTCCGGCCACC
CCATCTTGCGGTACCCCGGGCTCCGGGAGACGGCCACCTG
CACCCTGGAGGAGCTTCCCCACCTGGCCCGGGACCTGCCG                3120
CCCCGGTCTAGGGTCCTCCTTGCCGGGATGGTGGAGGAGG
TGGTGCGCAAGCCCACAAAGAGCGGCGGGATGATGGCCCG
CTTCGTCCTCTCCGACGAGACGGGGGCGCTTGAGGCGGTG                3240
GCATTCGGCCGGGCCTACGACCAGGTCTCCCCGAGGCTCA
AGGAGGACACCCCCGTGCTCGTCCTCGCCGAGGTGGAGCG
GGAGGAGGGGGGCGTGCGGGTGCTGGCCCAGGCCGTTTGG                3360
ACCTACGAGGAGCTGGAGCAGGTCCCCCGGGCCCTCGAGG
TGGAGGTGGAGGCCTCCCTCCTGGACGACCGGGGGGTGGC
CCACCTGAAAAGCCTCCTGGACGAGCACGCGGGGACCCTC                3480
CCCCTGTACGTCCGGGTCCAGGGCGCCTTCGGCGAGGCCC
TCCTCGCCCTGAGGGAGGTGCGGGTGGGGGAGGAGGCTGT
AGGCGGCCGCGTGGTTCCGGGCCTACCTCCTGCCCGACCG                3600
GGAGGTCCTTCTCCAGGGCGGCCAGGCGGGGGAGGCCCAG
GAGGCGGTGCCCTTCTAGGGGGTGGGCCGTGAGACCTAGC
GCCATCGTTCTCGCCGGGGGCAAGGAGGCCTGGGCCCGAC                3720
CCCTTTTGG
```

FIG. 16B

```
MGRELRFAHLHQHTQFSLLDGAPKLSDLLKWVEETTPEDP
ALAMTDHGNLFGAVEFYKKATEMGIKPILGYEAYVAAESR
FDRKRGKGLDGGYFHLTLLAKDFTGYQNLVRLASRAYLEG          120
FYEKPRIDREILREHAEGLIALSGCLGAEIPQFILQDRLD
LAEARLNEYLSIFKDRFFIEIQNHGLPEQKKVNEVLKEFA
RKYGLGMVATNDGHYVRKEDARAHEVLLAIQSKSTLDDPG          240
ALALPCEEFYVKTPEEMRAMFPEEEVGGRSPLTTPWRSPH
VQRGAAIGTRWSTRIPRFPLPEGRTEAQYLMELTFKGLLR
RYPDRITEGFYREVFRLSGKLPPHGDGEALAEALAQVERE          360
AWERLMKSLPPLAGVKEWTAEAIFHRALYELSAIERMGFP
GLLPHRPGLHQLGPEKGVSVGPGRGGAAGSLVAYAVGITN
IDPLRFGLLFERFLNPERVSMPDIDTDFSDRERDRVIQYV          480
RERYGEDKVAQIGTLGSLASKAALKEVARVYGIPRKKAEE
LAKLIPVQFGKPKPLQEAIQVVPELRAEMEKDPKVREVLE
VAMRLEGLNRHASVHAGRGGVFSEPLTDLVPLCATRKGGP          600
YTQYDMGAVEALGLLKMDFLGLRTLTFLDEVKRIVKASQG
VELDYDALPLDDPKTFALLSRGETKGVFQLESGGMTATLR
GLKPRRFEDLIAILSLYRPGPMEHIPTYIRRHHGLEPVSY          720
SEFPHAEKYLKPILDETYGIPVYQEQIMQIASAVAGYSLG
EADLLRRSMGKKKVEEMKSHRERFVQGAKERGVPEEEANR
LFDMLEAFANYGFNKSHAAAYSLLSYQTAYVKAHYPVEFM          840
AALLSVERHDSDKVAEYIRDARAMGIEVLPPDVNRSGFDF
LVQGRQILFGLSAVKNVGEAAAEAILRERERGGPYRSLGD
FLKRLDEKVLNKRTLESLIKAGALDGFGERARLLASLEGL          960
LKWAAENREKARSGMMGLFSEVEEPPLAEAAPLDEITRLR
YEKEALGIYVSGHPILRYPGLRETATCTLEELPHLARDLP
PRSRVLLAGMVEEVVRKPTKSGGMMARFVLSDETGALEAV         1080
AFGRAYDQVSPRLKEDTPVLVLAEVEREEGGVRVLAQAVW
TYQELEQVPRALEVEVEASLPDDRGVAHLKSLLDEHAGTL
PLYVRVQGAFGEALLALREVRVGEEALGALEAAGFPAYLL         1200
PNREVSPRLTGSGGPRGRALSTGLALKTYPIALPGGNEAL
ARPLL
```

FIG. 16C

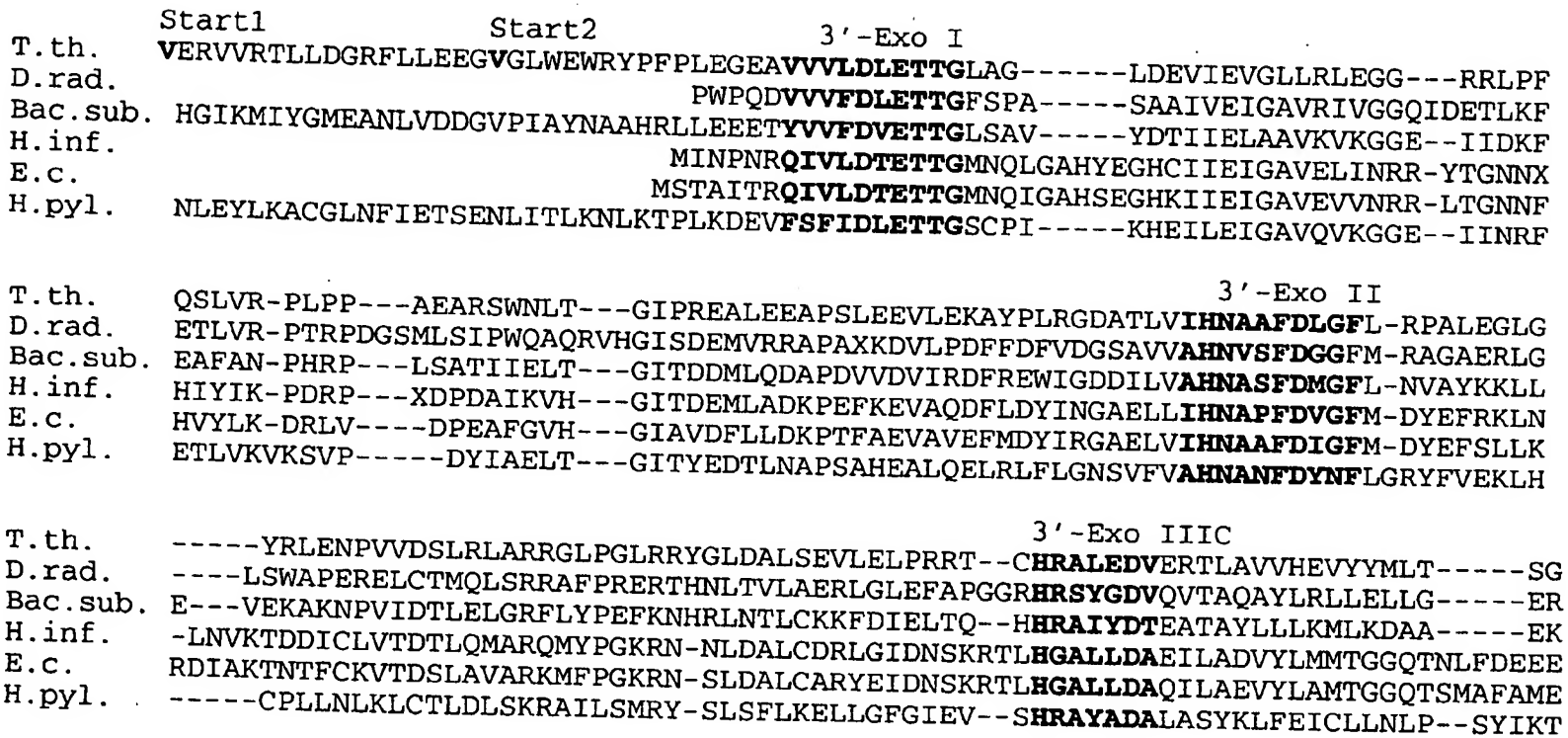

FIG. 17

REPLACEMENT SHEET
28/83

```
ATGGTGGAGCGGGTGGTGCGGACCCTTCTGGACGGGAGGT 40
TCCTCCTGGAGGAGGGGGTGGGGCTTTGGGAGTGGCGCTA
CCCCTTTCCCCTGGAGGGGGAGGCGGTGGTGGTCCTGGAC 120
CTGGAGACCACGGGGCTTGCCGGCCTGGACGAGGTGATTG
AGGTGGGCCTCCTCCGCCTGGAGGGGGGGAGGCGCCTCCC 200
CTTCCAGAGCCTCGTCCGGCCCCTCCCGCCCGCCGAAGCC
CGTTCGTGGAACCTCACCGGCATCCCCCGGGAGGCCCTGG 280
AGGAGGCCCCCTCCCTGGAGGAGGTTCTGGAGAAGGCCTA
CCCCCTCCGCGGCGACGCCACCTTGGTGATCCACAACGCC 360
GCCTTTGACCTGGGCTTCCTCCGCCCGGCCTTGGAGGGCC
TGGGCTACCGCCTGGAAAACCCCGTGGTGGACTCCCTGCG 440
CTTGGCCAGACGGGGCTTACCAGGCCTTAGGCGCTACGGC
CTGGACGCCCTCTCCGAGGTCCTGGAGCTTCCCCGAAGGA 520
CCTGCCACCGGGCCCTCGAGGACGTGGAGCGCACCCTCGC
CGTGGTGCACGAGGTATACTATATGCTTACGTCCGGCCGT 600
CCCCGCACGCTTTGGGAACTCGGGAGGTAG
```

FIG. 18A

```
MVERVVRTLLDGRFLLEEGVGLWEWRYPFPLEGEAVVVLD 40
LETTGLAGLDEVIEVGLLRLEGGRRLPFQSLVRPLPPAEA
RSWNLTGIPREALEEAPSLEEVLEKAYPLRGDATLVIHNA 120
AFDLGFLRPALEGLGYRLENPVVDSLRLARRGLPGLRRYG
LDALSEVLELPRRTCHRALEDVERTLAVVHEVYYMLTSGR 200
PRTLWELGRZ
```

FIG. 18B

REPLACEMENT SHEET

Alignment of dnaA genes.

```
P.mar.          MLEASWEK VQSSL--KQNLSK-- ----------PSYE TWIRPTEFSG--FKN GELTLIAPNSFSSAW LKNNYSQTIQETAE-     65
Syn.sp.       MVSCENLWQQ ALAIL--ATQLTK-- ----------PAFD TWIKASVLIS--LGD GVATIQVENGFVLNH LQKSYGPLLMEVLT-     67
B.sut.        MENILDLWNQ ALAQI--EKKLSK-- ----------PSFE TWMKSTKAHS--LQG DTLTITAPNEFARDW LESRYLHLIADTIY-     67
M.tub.  MTDDPGSGFTTVWNA VVSELNGDPKVDDGP SSDANLSAPLTPQQR AWLNLVQPLT--IVE GFALLSVPSSFVQNE IERHLRAPITDALS-     87
T.th.           MSHEAVWQH VLEHI--RRSITE-- ----------VEFH TWFERIRPLG--IRD GVLELAVPTSFALDW IRRHYAGLIQEGPR-     66
E.coli          MSLSLWQQ CLARL--QDELPA-- ----------TEFS MWIRPLQAE---LSD NTLALYAPNRFVLDW VRDKYLNNINGLLT-     64
T.mar.             MKER ILQEI--KTRVNR-- ----------KSWE LWFSSFDVKS--IEG NKVVFSVGNLFIKEW LEKKYYSVLSKAVK-     61
H.pyl.        MDTNNNIEKE ILALVKQNPKVSL-- ----------IEYE NYFSQLKYNPNASKS DIAFFYAPNQVLCTT ITAKYGALLKEILSQ     72

P.mar.   EIFG---EPVTVHVK VKANAESSDEHYSSA P--------------- ---ITPPLEASPGSV DSSGSSLRLSK---- -KTLPLLNLRYVFNR    130
Syn.sp.  DLTG---QEITVKLI TDGLEPHS---LIGQ E--------------- ---SSLPMETTP--- ---------------- -KNATALNGKYTFSR    115
B.sut.   ELTG---EELSIKFV IPQNQDVEDFMPKPQ VKKAVKEDTSDFPQN ---------------- ---------------- -----MLNPKYTFDT    119
M.tub.   RRLGH-QIQLGVRIA PPATDEADDTTVPPS ENPATTSPDTTTDND EIDDSAAARGDNQHS WPSYFTERPHNTDSA TAGVTSLNRRYTFDT    176
T.th.    LLGAQ-APRFELRVV PGVVVQEDIFQPPPS PPAQAQP-------- ---------------- ---------------- ---------EDTFKT    108
E.coli   SFCGADAPQLRFEVG TKPVTQTPQAAVTSN VAAPAQVAQTQPQRA APSTRSGWDNVPAPA EP-------------- -TYRSNVNVKHTFDN    140
T.mar.   VVLG---NDATFEIT YEAFEPHSSYSEPLV KKRAVLLTP------ ---------------- ---------------- ------LNPDYTFEN    106
H.pyl.   NKVG-MHLAHSVDVR IEVAPKIQINAQSNI NYKAIKTS------- ---------------- ---------------- ------VKDSYTFEN    118

P.mar.   FVVGPNSRMAHAAAM AVAESPGREFNPLFI CGGVGLGKTHLMQAI GHYRLEIDPGAKVSY VSTETFTNDLIL--A IRQDRMQAFRDRYR-    217
Syn.sp.  FVVGPTNRMAHAASL AVAESPGREFNPLFL CGGVGLGKTHLMQAI AHYRLEMYPNAKVYY VSTERFTNDLIT--A IRQDNMEDFRSYYR-    202
B.sut.   FVIGSGNRFAHAASL AVAEAPAKAYNPLFI YGGVGLGKTHLMHAI GHYVIDHNPSAKVVY LSSEKFTNEFIN--S IRDNKAVDFRNRYR-    206
M.tub.   FVIGASNRFAHAAAL AIAEAPARAYNPLFI WGESGLGKTHLLHAA GNYAQRLFPGMRVKY VSTEEFTNDFIN--S LRDDRKVAFKRSYR-    263
T.th.    SWWGPTTPWPHGGAV AVAESPGRAYNPLFI YGGRGLGKTYLMHAV GPLRAKRFPHMRLEY VSTETFTNELINRPS AR-DRMTEFRERYR-    196
E.coli   FVEGKSNQLARAAAR QVADNPGGAYNPLFL YGGTGLGKTHLLHAV GNGIMARKPNAKVVY MHSERFVQDMVK--A LQNNAIEEFKRYYR-    227
T.mar.   FVVGPGNSFAYHAAL EVAKHPGR-YNPLFI YGGVGLGKTHLLQSI GNYVVQNEPDLRVMY ITSEKFLNDLVD--S MKEGKLNEFREKYRK    193
H.pyl.   FVVGSCNNTVYEIAK KVAQSDTPPYNPVLF YGGTGLGKTHILNAI GNHALEK--HKKVVL VTSEDFLTDFLK--H LDNKTMDSFKAKYR-    203
```

FIG. 19A

REPLACEMENT SHEET

```
P.mar.   AADLILVDDIQFIEG KEYTQEEFFHTFNAL HDAGSQIVLASDRPP SQIPRLQERLMSRFS MGLIADVQAPDLETR MAILQKKAEHERVGL    307
Syn.sp.  SADFLLIDDIQFIKG KEYTQEEFFHTFNSL HEAGKQVVVASDRAP QRIPGLQDRLISRFS MGLIADIQVPDLETR MAILQKKAEYDRIRL    292
B.sut.   NVDVLLIDDIQFLAG KEQTQEEFFHTFNTL HEESKQIVISSDRPP KEIPTLEDRLRSRFE WGLITDITPPDLETR IAILRKKAKAEGLDI    296
M.tub.   DVDVLLVDDIQFIEG KEGIQEEFFHTFNTL HNANKQIVISSDRPP KQLATLEDRLRTRFE WGLITDVQPPELETR IAILRKKAQMERLAV    353
T.th.    SVDLLLVDDVQFIAG KERTQEEFFHTFNAL YEAHKQIILSSDRPP KDILTLEARLRSRFE WGLITDNPAPDLETR IAILKMNAS-SGPED    285
E.coli   SVDALLIDDIQFFAN KERSQEEFFHTFNAL LEGNQQIILTSDRYP KEINGVEDRLKSRFG WGLTVAIEPPELETR VAILMKKADENDIRL    317
T.mar.   KVDILLIDDVQFLIG KTGVQTELFHTFNEL HDSGKQIVICSDREP QKLSEFQDRLVSRFQ MGLVAKLEPPDEETR KSIARKMLEIEHGEL    283
H.pyl.   HCDFFLLDDAQFLQG KPKLEEEFFHTFNEL HANSKQIVLISDRSP KNIAGLEDRLKSRFE WGITAKVMPPDLETK LSIVKQKCQLNQITL    293

P.mar.   PRDLIQFIAGRFTSN IRELEGALTRAIAFA SITGLPMTVDSIAPM LD----PNGQGVEVT PKQVLDKVAEVFKVT PDEMRSASRRR-PVS    392
Syn.sp.  PKEVIEYIASHYTSN IRELEGALIRAIAYT SLSNVAMTVENIAPV LN----PPVEKVAAA PETIITIVAQHYQLK VEELLSNSRRR-EVS    377
B.sut.   PNEVMLYIANQIDSN IRELEGALIRVVAYS SLINKDINADLAAEA LKDII-PSSKPKVIT IKEIQRVVGQQFNIK LEDFKAKKRTK-SVA    384
M.tub.   PDDVLELIASSIERN IRELEGALIRVTAFA SLNKTPIDKALAEIV LRDLI-ADANTMQIS AATIMAATAEYFDTT VEELRGPGKTR-ALA    441
T.th.    PEDALEYIARQVTSN IREWEGALMRASPFA SLNGVELTRAVAAKA LRHLR-P--RELEAD PLEIIRKAAGPVRPE TPGGAHGERRKKEVV    372
E.coli   PGEVAFFIAKRLRSN VRELEGALNRVIANA NFTGRAITIDFVREA LRDLL-A-LQEKLVT IDNIQKTVAEYYKIK VADLLSKRRSR-SVA    404
T.mar.   PEEVLNFVAENVDDN LRRLRGAIIKLLVYK ETTGKEVDLKEAILL LKDFIKPNRVKAMDP IDELIEIVAKVTGVP REEILSNSRNV-KAL    372
H.pyl.   PEEVMEYIAQHISDN IRQMEGAIIKISVNA NLMNASIDLNLAKTV LEDL--QKDHAEGSS LENILLAVAQSLNLK SSEIKVSSRQK-NVA    380

P.mar.   QARQVGMYLMRQGTN LSLPRIGDTFGGKDH TTVMYAIEQVEKKLS S---------DPQIA SQVQKIRDLLQIDSR RKR----    461
Syn.sp.  LARQVGMYLMRQHTD LSLPRIGEAFGGKDH TTVMYSCDKITQLQQ K---------DWETS QTLTSLSHRINIAGQ APES---    447
B.sut.   FPRQIAMYLSREMTD SSLPKIGEEFGGRDH TTVIHAHEKISKLLA D---------DEQLQ QHVKEIKEQLK---- -------    446
M.tub.   QSRQIAMYLCRELTD LSLPKIGQAFG-RDH TTVMYAQRKILSEMA E---------RREVF DHVKELTTRIRQRSK R------    507
T.th.    LPRQLAMYLVRELTP ASLPEIGQLFGGRDH TTVRYAIQKVQELAG KP--------DREVQ GLLRTLREACTDPVD NLWITCG    446
E.coli   RPRQMAMALAKELTN HSLPEIGDAFGGRDH TTVLHACRKIEQLRE E---------SHDIK EDFSNLIRTLSS--- -------    467
T.mar.   TARRIGMYVAKNYLK SSLRTIAEKFN-RSH PVVVDSVKKVKDSLL KG--------NKQLK ALIDEVIGEISRRAL SG-----    440
H.pyl.   LARKLVVYFARLYTP NPTLSLAQFLDLKDH SSISKMYSGVKKMLE EEKSPFVLSLREEIK NRLNELNDKKTAFNS SE-----    457
```

FIG. 19B

GTGTCGCACGAGGCCGTCTGGCAACACGTTCTGGAGCACA
TCCGCCGCAGCATCACCGAGGTGGAGTTCCACACCTGGTT
TGAAAGGATCCGCCCCTTGGGGATCCGGGACGGGGTGCTG 120
GAGCTCGCCGTGCCCACCTCCTTTGCCCTGGACTGGATCC
GGCGCCACTACGCCGGCCTCATCCAGGAGGGCCCTCGGCT
CCTCGGGGCCCAGGCGCCCCGGTTTGAGCTCCGGGTGGTG 240
CCCGGGGTCGTAGTCCAGGAGGACATCTTCCAGCCCCCGC
CGAGCCCCCCGGCCCAAGCTCAACCCGAAGATACCTTTAA
AACTTCGTGGTGGGGCCCAACAACTCCATGGCCCCACGGC 360
GGCGCCGTGGCCGTGGCCGAGTCCCCCGGCCGGGCCTACA
ACCCCCTCTTCATCTACGGGGGCCGTGGCCTGGGAAAGAC
CTACCTGATGCACGCCGTGGGCCCACTCCGTGCGAAGCGC 480
TTCCCCCACATGAGATTAGAGTACGTTTCCACGGAAACTT
TCACCAACGAGCTCATCAACCGGCCATCCGCGAGGGACCG
GATGACGGAGTTCCGGGAGCGGTACCGCTCCGTGGACCTC 600
CTGCTGGTGGACGACGTCCAGTTCATCGCCGGAAAGGAGC
GCACCCAGGAGGAGTTTTTCCACACCTTCAACGCCCTTTA
CGAGGCCCACAAGCAGATCATCCTCTCCTCCGACCGGCCG 720
CCCAAGGACATCCTCACCCTGGAGGCGCGCCTGCGGAGCC
GCTTTGAGTGGGGCCTGATCACCGACAATCCAGCCCCCGA
CCTGGAAACCCGGATCGCCATCCTGAAGATGAACGCCAGC 840
AGCGGGCCTGAGGATCCCGAGGACGCCCTGGAGTACATCG
CCCGGCAGGTCACCTCCAACATCCGGGAGTGGGAAGGGGC
CCTCATGCGGGCATCGCCTTTCGCCTCCCTCAACGGCGTT 960
GAGCTGACCCGCGCCGTGGCGGCCAAGGCTCTCCGACATC
TTCGCCCCAGGGAGCTGGAGGCGGACCCCTTGGAGATCAT
CCGCAAAGCGGCGGGACCAGTTCGGCCTGAAACCCCGGGA 1080
GGAGCTCACGGGGAGCGCCGCAAGAAGGAGGTGGTCCTCC
CCCGGCAGCTCGCCATGTACCTGGTGCGGGAGCTCACCCC
GGCCTCCCTGCCCGAGATCGACCAGCTCAACGACGACCGG 1200
GACCACACCACGGTCCTCTACGCCATCCAGAAGGTCCAGG
AGCTCGCGGAAAGCGACCGGGAGGTGCAGGGCCTCCTCCG
CACCCTCCGGGAGGCGTGCACATGA

FIG. 20A

```
VSHEAVWQHVLEHIRRSITEVEFHTWFERIRPLGIRDGVL
ELAVPTSFALDWIRRHYAGLIQEGPRLLGAQAPRFELRVV
PGVVVQEDIFQPPPSPPAQAQPEDTFKTSWWGPTTPWPHG 120
GAVAVAESPGRAYNPLFIYGGRGLGKTYLMHAVGPLRAKR
FPHMRLEYVSTETFTNELINRPSARDRMTEFRERYRSVDL
LLVDDVQFIAGKERTQEEFFHTFNALYEAHKQIILSSDRP 240
PKDILTLEARLRSRFEWGLITDNPAPDLETRIAILKMNAS
SGPEDPEDALEYIARQVTSNIREWEGALMRASPFASLNGV
ELTRAVAAKALRHLRPRELEADPLEIIRKAAGPVRPETPG 360
GAHGERRKKEVVLPRQLAMYLVRELTPASLPEIDQLNDDR
DHTTVLYAIQKVQELAESDREVQGLLRTLREACT
```

FIG. 20B

```
ATGAACATAACGGTTCCCAAAAAACTCCTCTCGGACCAGC  40
TTTCCCTCCTGGAGCGCATCGTCCCCTCTAGAAGCGCCAA
CCCCCTCTACACCTACCTGGGGCTTTACGCCGAGGAAGGG 120
GCCTTGATCCTCTTCGGGACCAACGGGGAGGTGGACCTCG
AGGTCCGCCTCCCCGCCGAGGCCCAAAGCCTTCCCCGGGT 200
GCTCGTCCCCGCCCAGCCCTTCTTCCAGCTGGTGCGGAGC
CTTCCTGGGGACCTCGTGGCCCTCGGCCTCGCCTCGGAGC 280
CGGGCCAGGGGGGGCAGCTGGAGCTCTCCTCCGGGCGTTT
CCGCACCCGGCTCAGCCTGGCCCCTGCCGAGGGCTACCCC 360
GAGCTTCTGGTGCCCGAGGGGGAGGACAAGGGGGCCTTCC
CCCTCCGGACGCGGATGCCCTCCGGGGAGCTCGTCAAGGC 440
CTTGACCCACGTGCGCTACGCCGCGAGCAACGAGGAGTAC
CGGGCCATCTTCCGCGGGGTGCAGCTGGAGTTCTCCCCCC 520
AGGGCTTCCGGGCGGTGGCCTCCGACGGGTACCGCCTCGC
CCTCTACGACCTGCCCCTGCCCCAAGGGTTCCAGGCCAAG 600
GCCGTGGTCCCCGCCCGGAGCGTGGACGAGATGGTGCGGG
TCCTGAAGGGGGCGGACGGGGCCGAGGCCGTCCTCGCCCT 680
GGGCGAGGGGGTGTTGGCCCTGGCCCTCGAGGGCGGAAGC
GGGGTCCGGATGGCCCTCCGCCTCATGGAAGGGGAGTTCC 760
CCGACTACCAGAGGGTCATCCCCCAGGAGTTCGCCCTCAA
GGTCCAGGTGGAGGGGGAGGCCCTCAGGGAGGCGGTGCGC 840
CGGGTGAGCGTCCTCTCCGACCGGCAGAACCACCGGGTGG
ACCTCCTTTTGGAGGAAGGCCGGATCCTCCTCTCCGCCGA 920
GGGGGACTACGGCAAGGGGCAGGAGGAGGTGCCCGCCCAG
GTGGAGGGGCCGGACATGGCCGTGGCCTACAACGCCCGCT 1000
ACCTCCTCGAGGCCCTCGCCCCCGTGGGGGACCGGGCCCA
CCTGGGCATCTCCGGGCCCACGAGCCCGAGCCTCATCTGG 1080
GGGGACGGGGAGGGGTACCGGGCGGTGGTGGTGCCCCTCA
GGGTCTAG                                  1128
```

FIG. 21A

```
MNITVPKKLLSDQLSLLERIVPSRSANPLYTYLGLYAEEG 40
ALILFGTNGEVDLEVRLPAEAQSLPRVLVPAQPFFQLVRS
LPGDLVALGLASEPGQGGQLELSSGRFRTRLSLAPAEGYP 120
ELLVPEGEDKGAFPLRTRMPSGELVKALTHVRYAASNEEY
RAIFRGVQLEFSPQGFRAVASDGYRLALYDLPLPQGFQAK 200
AVVPARSVDEMVRVLKGADGAEAVLALGEGVLALALEGGS
GVRMALRLMEGEFPDYQRVIPQEFALKVQVEGEALREAVR 280
RVSVLSDRQNHRVDLLLEEGRILLSAEGDYGKGQEEVPAQ
VEGPDMAVAYNARYLLEALAPVGDRAHLGISGPTSPSLIW 360
GDGEGYRAVVVPLRVZ
```

FIG. 21B

```
T.th.beta       MNITVPKKLLSDQLSLLERIVPSRSANPLYTYLGLYAEEGALILFGTNGEVDLEVRLPAE
E.coli.bet      MKFTVEREHLLKPLQQVSGPLGGRPTLPILGNLLLQVADGTLSLTGTDLEMEMVARVALV
P.mirab.be      MKFIIEREQLLKPLQQVSGPLGGRPTLPILGNLLLKVTENTLSLTGTDLEMEMMARVSLS
H.infl.bet      MQFSISRENLLKPLQQVCGVLSNRPNIPVLNNVLLQIEDYRLTITGTDLEVELSSQTQLS
P.put.beta      MHFTIQREALLKPLQLVAGVVERRQTLPVLSNVLLVVQGQQLSLTGTDLEVELVGRVQLE
B.cap.beta      MKFTIQNDILTKNLKKITRVLVKNISFPILENILIQVEDGTLSLTTTNLEIELISKIEII
                *   .   *   *  .  .      *. . . .      * . * *... .

T.th.beta       AQSLP-RVLVPAQPFFQLVRSLPGDLVALGLASEPGQGGQLELSSGRFRTRLSLAPAEGY
E.coli.bet      QPHEPGATTVPARKFFDICRGLP-EGAEIAVQLE---GERMLVRSGRSRFSLSTLPAADF
P.mirab.be      QSHEIGATTVPARKFFDIWRGLP-EGAEISVELD---GDRLLVRSGRSRFSLSTLPASDF
H.infl.bet      SSSENGTFTIPAKKFLDICRTLS-DDSEITVTFE---QDRALVQSGRSRFTLATQPAEEY
P.put.beta      EPAEPGEITVPARKLMDICKSLP-NDALIDIKVD---EQKLLVKAGRSRFTLSTLPANDF
B.cap.beta      TKYIPGKTTISGRKILNICRTLS-EKSKIKMQLK---NKKMYISSENSNYILSTLSADTF
                        . .   . . *     . .       . . .       *.  *  .

T.th.beta       PELLVPEGEDKGAFPLRTRMPSGELVKALTHVRYAASNEEYRAIFRGVQLEFSPQGFRAV
E.coli.bet      PNLDD--WQSEVEFTLPQAT----MKRLIEATQFSMAHQDVRYYLNGMLFETEGEELRTV
P.mirab.be      PNLDD--WQSEVEFTLPQAT----LKRLIESTQFSMAHQDVRYYLNGMLFETENTELRTV
H.infl.bet      PNLTD--WQSEVDFELPQNT----LRRLIEATQFSMANQDARYFLNGMKFETEGNLLRTV
P.put.beta      PTVEE--GPGSLTCNLEQSK----LRRLIERTSFAMAQQDVRYYLNGMLLEVSRNTLRAV
B.cap.beta      PNHQN--FDYISKFDISSNI----LKEMIEKTEFSMGKQDVRYYLNGMLLEKKDKFLRSV
                *                .   .  .  .. .. *   *.  *     *.*

T.th.beta       ASDGYRLALYDLPLPQGFQA--KAVVPARSVDEMVRVLKGADGAEAVLALGEGVLALALE
E.coli.bet      ATDGHRLAVCSMPIGQSLPS-HSVIVPRKGVIELMRMLDG-GDNPLRVQIGSNNIRAHVG
P.mirab.be      ATDGHRLAVCAMDIGQSLPG-HSVIVPRKGVIELMRLLDGSGESLLQLQIGSNNLRAHVG
H.infl.bet      ATDGHRLAVCTISLEQELQN-HSVILPRKGVLELVRLLET-NDEPARLQIGTNNLRVHLK
P.put.beta      STDGHRLALCSMSAPIEQEDRHQVIVPRKGILELARLLTD-PEGMVSIVLGQHHIRATTG
B.cap.beta      ATDGYRLAISYTQLKKDINF-FSIIIPNKAVMELLKLLNT-QPQLLNILIGSNSIRIYTK
                ..** ***.                ..* . . *. ..*         . .*   .
```

FIG. 22A

REPLACEMENT SHEET

36/83

```
T.th.beta      GGSGVRMALRLMEGEFPDYQRVIPQEFALKVQVEGEALREAVRRVSVLSDRQNHRVDLLL
E.coli.bet     ---DFIFTSKLVDGRFPDYRRVLPKNPDKHLEAGCDLLKQAFARAAILSNEKFRGVRLYV
P.mirab.be     ---DFIFTSKLVDGRFPDYRRVLPKNPTKTVIAGCDILKQAFSRAAILSNEKFRGVRINL
H.infl.bet     ---NTVFTSKLIDGRFPDYRRVLPRNATKIVEGNWEMLKQAFARASILSNERARSVRLSL
P.put.beta     ---EFTFTSKLVDGKFPDYERVLPKGGDKLVVGDRQALREAFSRTAILSNEKYRGIRLQL
B.cap.beta     ---NLIFTTQLIEGEYPDYKSVLFKEKKNPIITNSILLKKSLLRVAILAHEKFCGIEIKI
                     . .*..* .***  *. .     .        *. .  * ..*.  .  . . .

T.th.beta      EEGRILLSAEGDYGK-GQEEVPAQVEGPDMAVAYNARYLLEALAPVG-DRAHLGISGPTS
E.coli.bet     SENQLKITANNPEQEEAEEILDVTYSGAEMEIGFNVSYVLDVLNALKCENVRMMLTDSVS
P.mirab.be     TNGQLKITANNPEQEEAEEIVDVQYQGEEMEIGFNVSYLLDVLNTLKCEEVKLLLTDAVS
H.infl.bet     KENQLKITASNTEHEEAEEIVDVNYNGEELEVGFNVTYILDVLNALKCNQVRMCLTDAFS
P.put.beta     AAGQLKIQANNPEQEEAEEEISVDYEGSSLEIGFNVSYLLDVLGVMTTEQVRLILSDSNS
B.cap.beta     ENGKFKVLSDNQEEETAEDLFEIDYFGEKIEISINVYYLLDVINNIKSENIALFLNKSKS
                 .. . . .       ..       *  . .  *  *.*. . .        . .    *

T.th.beta      PSLIWGDG-EGYRAVVVPLRVZ     (ID#108)
E.coli.bet     SVQIEDAASQSAAYVVMPMRLZ     (ID#109)
P.mirab.be     SVQVENVASAAAAYVVMPMRL-     (ID#110)
H.infl.bet     SCLIENCEDSSCEYVIMPMRL-     (ID#111)
P.put.beta     SALLQEAGNDDSSYVVMPMRL-     (ID#112)
B.cap.beta     SIQIEAENNSSNAYVVMLLKR-     (ID#113)
                  .          *.. ..
```

FIG. 22B

REPLACEMENT SHEET

37/83

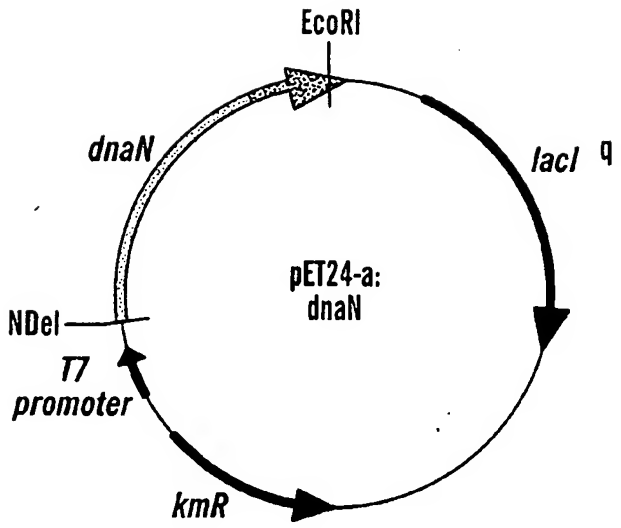

FIG. 23

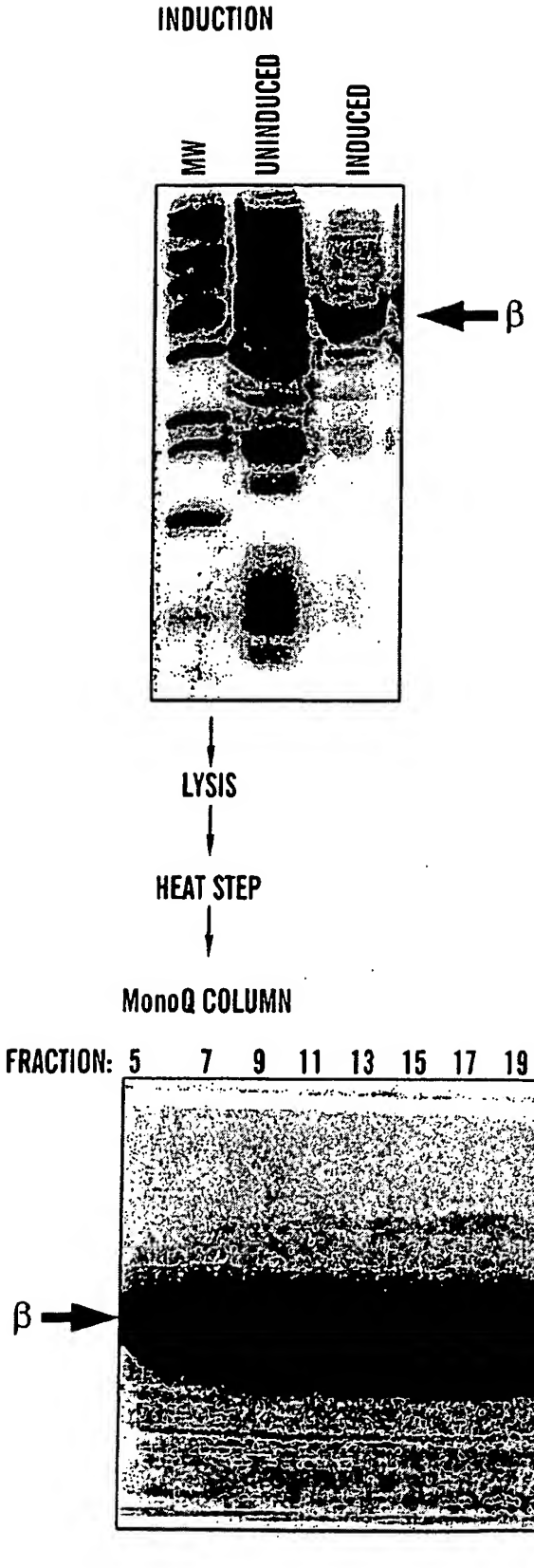

FIG. 24A

FIG. 24B

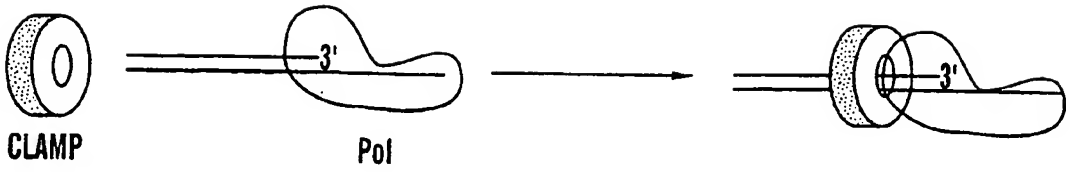

FIG. 25A

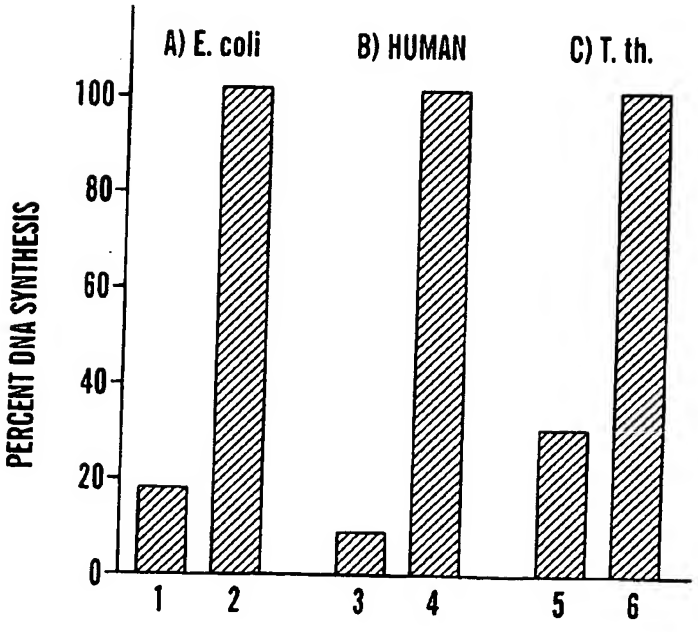

FIG. 25B

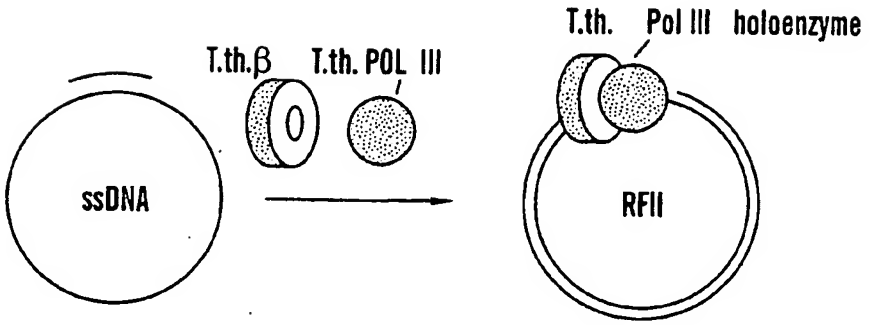

FIG. 26A

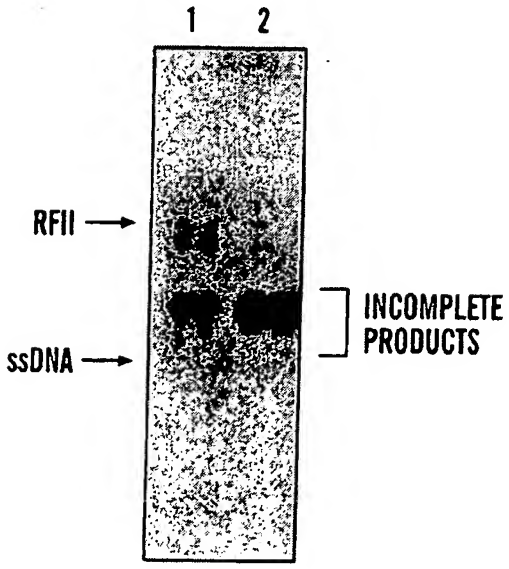

FIG. 26B

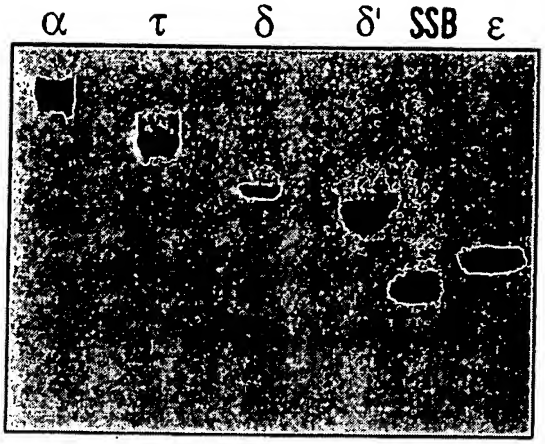
α
τ
δ
δ'
SSB
ε

FIG. 27

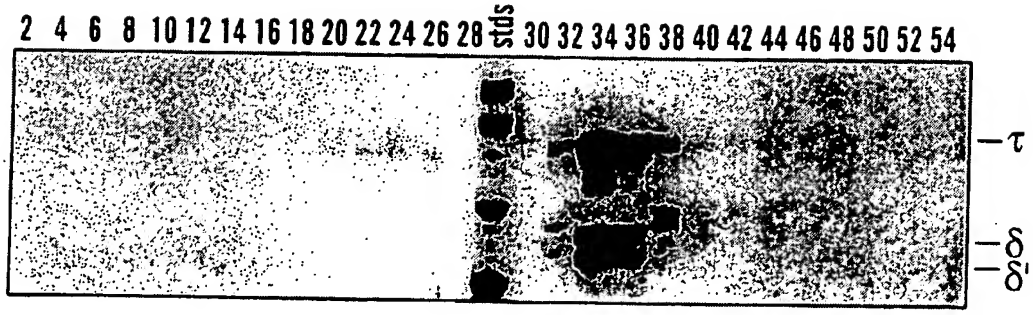
2 4 6 8 10 12 14 16 18 20 22 24 26 28
stds
30 32 34 36 38 40 42 44 46 48 50 52 54
τ
δ
δ'

FIG. 28

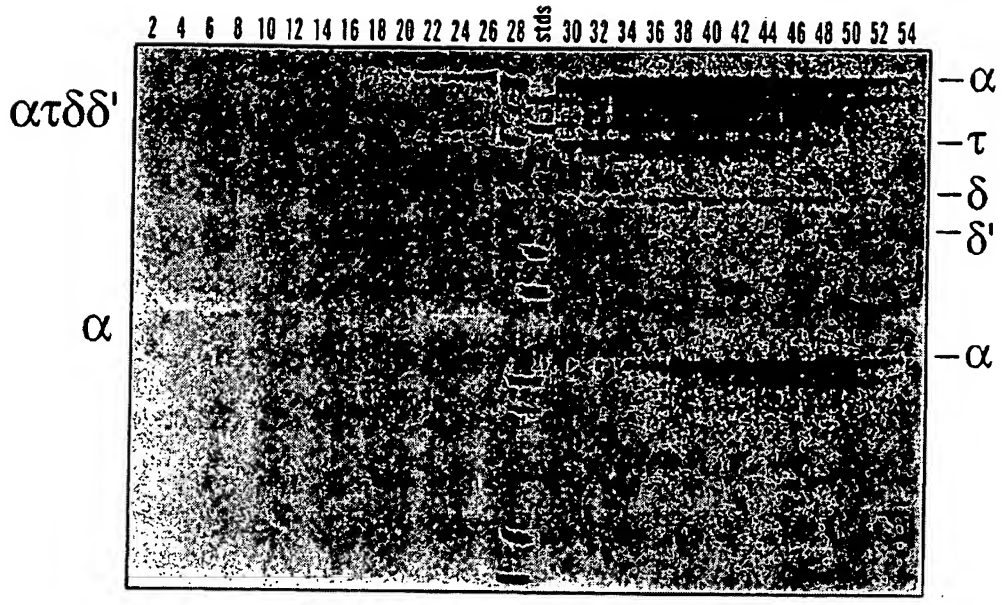
2 4 6 8 10 12 14 16 18 20 22 24 26 28 stds 30 32 34 36 38 40 42 44 46 48 50 52 54
αταδδ'
α
α
τ
δ
δ'
α

FIG. 29

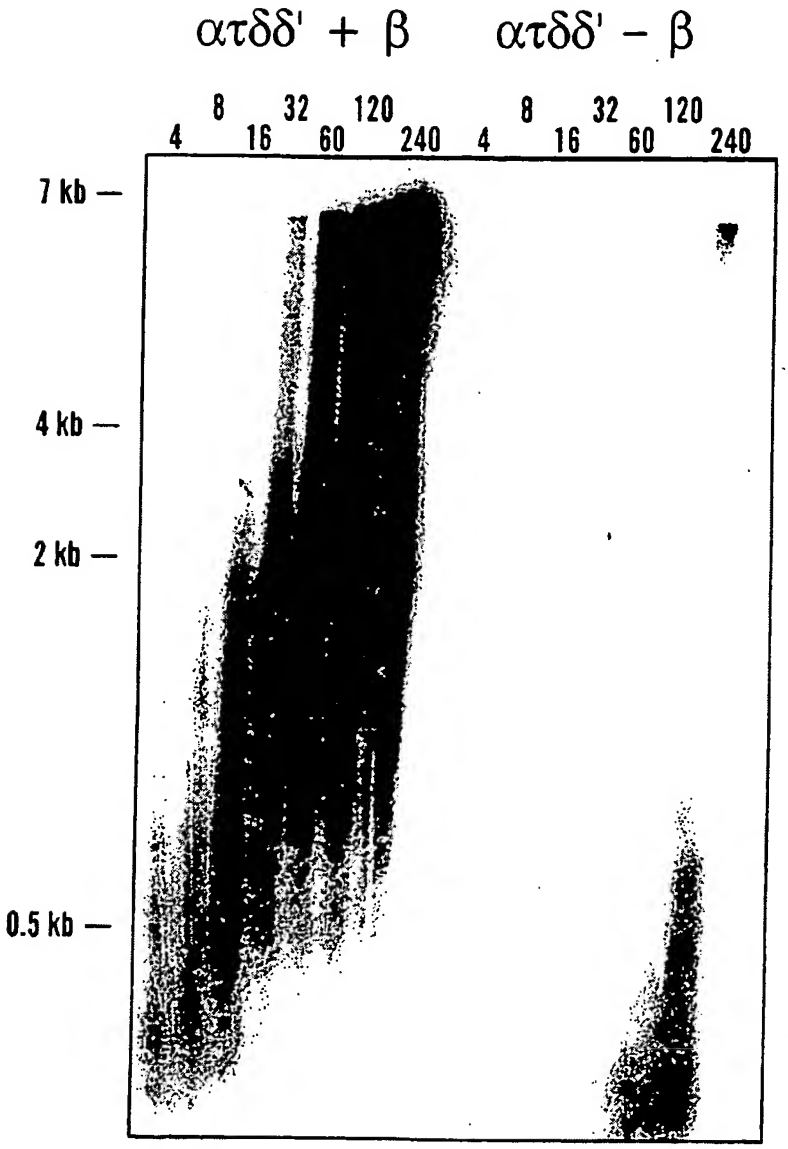
αταδδ' + β
αταδδ' − β
4
8
16
32
60
120
240
4
8
16
32
60
120
240
7 kb
4 kb
2 kb
0.5 kb

FIG. 30

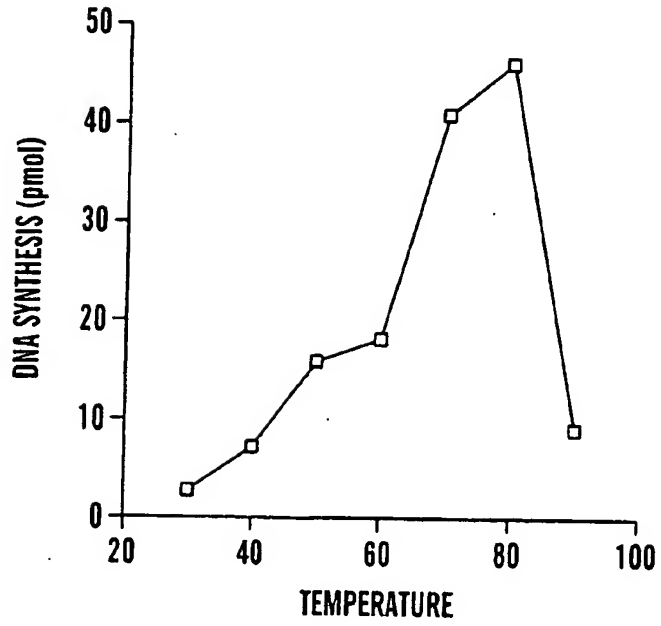
DNA SYNTHESIS (pmol)
50
40
30
20
10
0
20
40
60
80
100
TEMPERATURE

FIG. 31

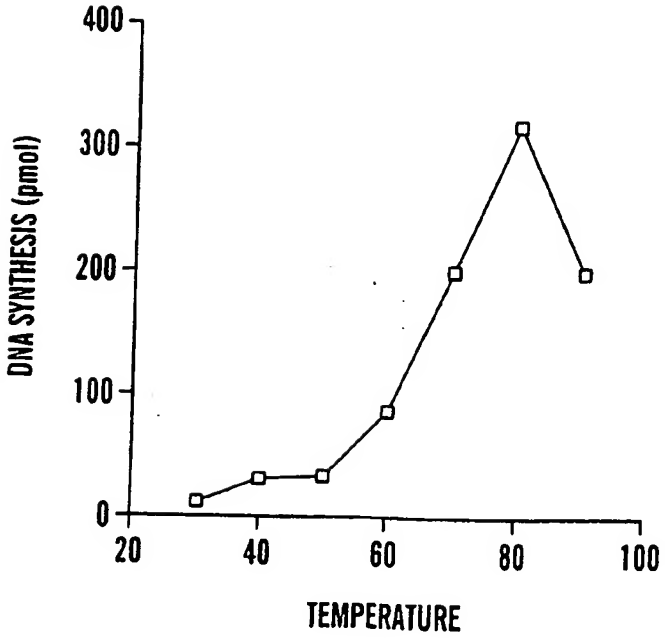
DNA SYNTHESIS (pmol)
400
300
200
100
0
20
40
60
80
100
TEMPERATURE

FIG. 32

α

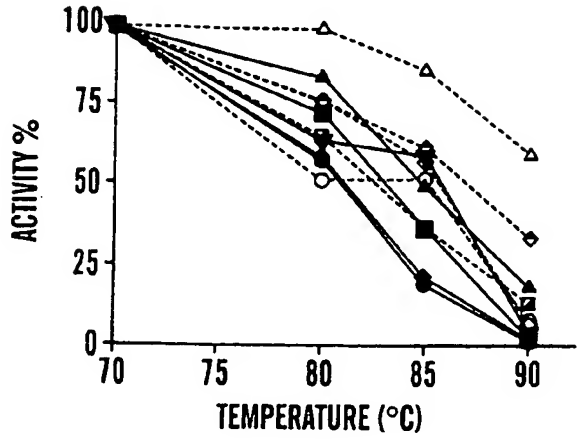

FIG. 33A

β

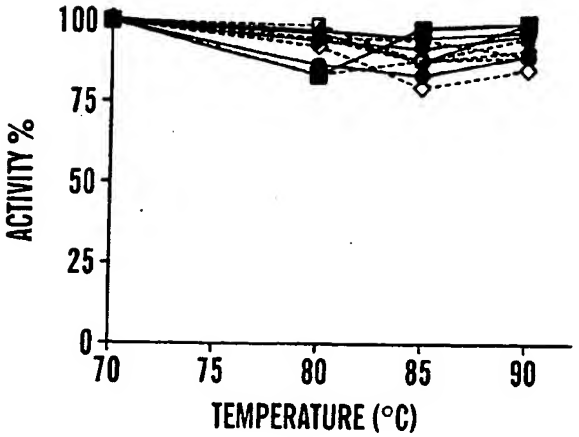

FIG. 33B

τδδ'

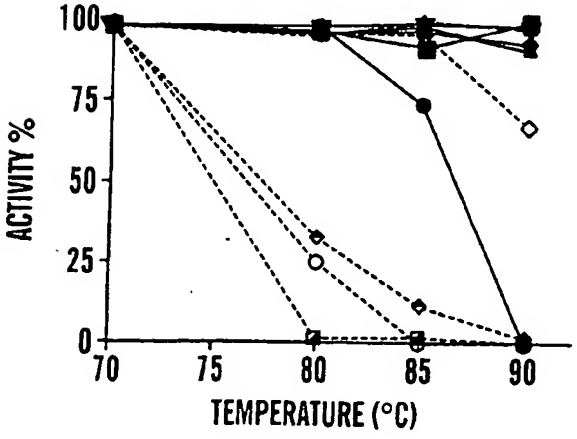

FIG. 33C

SSB

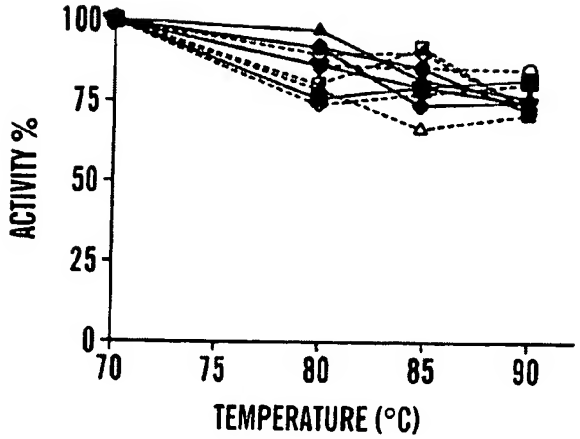

FIG. 33D

Pol III*

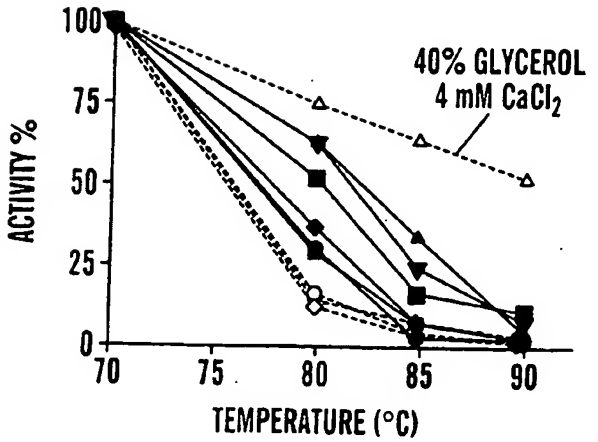

FIG. 33E

```
ATGAGTAAGGATTTCGTCCACCTTCACCTGCACACCCAGTTCTCACTCCT
GGACGGGGCTATAAAGATAGACGAGCTCGTGAAAAAGGCAAAGGAGTATG    100
GATACAAAGCTGTCGGAATGTCAGACCACGGAAACCTCTTCGGTTCGTAT
AAATTCTACAAAGCCCTGAAGGCGGAAGGAATTAAGCCCATAATCGGCAT    200
GGAAGCCTACTTTACCACGGGTTCGAGGTTTGACAGAAAGACTAAAACGA
GCGAGGACAACATAACCGACAAGTACAACCACCACCTCATACTTATAGCA    300
AAGGACGAAAAGGTCTAAAGAACTTAATGAAGCTCTCAACCCTCGCCTAC
AAAGAAGGTTTTTACTACAAACCCAGAATTGATTACGAACTCCTTGAAAA    400
GTACGGGGAGGGCCTAATAGCCCTTACCGCATGCCTGAAAGGTGTTCCCA
CCTACTACGCTTCTATAAACGAAGTGAAAAAGGCGGAGGAATGGGTAAAG    500
AAGTTCAAGGATATATTCGGAGATGACCTTTATTTAGAACTTCAAGCGAA
CAACATTCCAGAACAGGAAGTGGCAAACAGGAACTTAATAGAGATAGCCA    600
AAAAGTACGATGTGAAACTCATAGCGACGCAGGACGCCCACTACCTCAAT
CCCGAAGACAGGTACGCCCACACGGTTCTTATGGCACTTCAAATGAAAAA    700
GACCATTCACGAACTGAGTTCGGGAAACTTCAAGTGTTCAAACGAAGACC
TTCACTTTGCTCCACCCGAGTACATGTGGAAAAAGTTTGAAGGTAAGTTC    800
GAAGGCTGGGAAAAGGCACTCCTGAACACTCTCGAGGTAATGGAAAAGAC
AGCGGACAGCTTTGAGATATTTGAAAACTCCACCTACCTCCTTCCCAAGT    900
ACGACGTTCCGCCCGACAAAACCCTTGAGGAATACCTCAGAGAACTCGCG
TACAAAGGTTTAAGACAGAGGATAGAAAGGGGACAAGCTAAGGATACTAA   1000
AGAGTACTGGGAGAGGCTCGAGTACGAACTGGAAGTTATAAACAAAATGG
GCTTTGCGGGATACTTCTTGATAGTTCAGGACTTCATAAACTGGGCTAAG   1100
AAAAACGACATACCTGTTGGACCCGGAAGGGGAAGTGCTGGAGGTTCCCT
CGTCGCATACGCCATCGGAATAACGGACGTTGACCCTATAAAGCACGGAT   1200
TCCTTTTTGAGAGGTTCTTAAACCCCGAAAGGGTTTCCATGCCGGATATA
GACGTGGATTTCTGTCAGGACAACAGGGAAAAGGTCATAGAGTACGTAAG   1300
GAACAAGTACGGACACGACAACGTAGCTCAGATAATCACCTACAACGTAA
TGAAGGCGAAGCAAACACTGAGAGACGTCGCAAGGGCCATGGGACTCCCC   1400
TACTCCACCGCGGACAAACTCGCAAAACTCATTCCTCAGGGGGACGTTCA
GGGAACGTGGCTCAGTCTGGAAGAGATGTACAAAACGCCTGTGGAGGAAC   1500
TCCTTCAGAAGTACGGAGAACACAGAACGGACATAGAGGACAACGTAAAG
AAGTTCAGACAGATATGCGAAGAAAGTCCGGAGATAAAACAGCTCGTTGA   1600
GACGGCCCTGAAGCTTGAAGGTCTCACGAGACACACCTCCCTCCACGCCG
CGGGAGTGGTTATAGCACCAAAGCCCTTGAGCGAGCTCGTTCCCCTCTAC   1700
TACGATAAAGAGGGCGAAGTCGCAACCCAGTACGACATGGTTCAGCTCGA
AGAACTCGGTCTCCTGAAGATGGACTTCCTCGGACTCAAAACCCTCACAG   1800
AACTGAAACTCATGAAAGAACTCATAAAGGAAAGACACGGAGTGGATATA
AACTTCCTTGAACTTCCCCTTGACGACCCGAAAGTTTACAAACTCCTTCA   1900
GGAAGGAAAAACCACGGGAGTGTTCCAGCTCGAAAGCAGGGGAATGAAAG
AACTCCTGAAGAAACTAAAGCCCGACAGCTTTGACGACATCGTTGCGGTC   2000
CTCGCACTCTACAGACCCGGACCTCTAAAGAGCGGACTCGTTGACACATA
CATTAAGAGAAAGCACGGAAAAGAACCCGTTGAGTACCCCTTCCCGGAGC   2100
TTGAACCCGTCCTTAAGGAAACCTACGGAGTAATCGTTTATCAGGAACAG
GTGATGAAGATGTCTCAGATACTTTCCGGCTTTACTCCCGGAGAGGCGGA   2200
TACCCTCAGAAAGGCGATAGGTAAGAAGAAAGCGGATTTAATGGCTCAGA
TGAAAGACAAGTTCATACAGGGAGCGGTGGAAAGGGGATACCCTGAAGAA   2300
AAGATAAGGAAGCTCTGGGAAGACATAGAGAAGTTCGCTTCCTACTCCTT
CAACAAGTCTCACTCGGTAGCTTACGGGTACATCTCCTACTGGACCGCCT   2400
```

FIG. 34A

ACGTTAAAGCCCACTATCCCGCGGAGTTCTTCGCGGTAAAACTCACAACT
GAAAAGAACGACAACAAGTTCCTCAACCTCATAAAAGACGCTAAACTCTT 2500
CGGATTTGAGATACTTCCCCCCGACATAAACAAGAGTGATGTAGGATTTA
CGATAGAAGGTGAAAACAGGATAAGGTTCGGGCTTGCGAGGATAAAGGGA 2600
GTGGGAGAGGAAACTGCTAAGATAATCGTTGAAGCTAGAAAGAAGTATAA
GCAGTTCAAAGGGCTTGCGGACTTCATAAACAAAACCAAGAACAGGAAGA 2700
TAAACAAGAAAGTCGTGGAAGCACTCGTAAAGGCAGGGGCTTTTGACTTT
ACTAAGAAAAAGAGGAAAGAACTACTCGCTAAAGTGGCAAACTCTGAAAA 2800
AGCATTAATGGCTACACAAAACTCCCTTTTCGGTGCACCGAAAGAAGAAG
TGGAAGAACTCGACCCCTTAAAGCTTGAAAAGGAAGTTCTCGGTTTTTAC 2900
ATTTCAGGGCACCCCCTTGACAACTACGAAAAGCTCCTCAAGAACCGCTA
CACACCCATTGAAGATTTAGAAGAGTGGGACAAGGAAAGCGAAGCGGTGC 3000
TTACAGGAGTTATCACGGAACTCAAAGTAAAAAAAGACGAAAAACGGAGAT
TACATGGCGGTCTTCAACCTCGTTGACAAGACGGGACTAATAGAGTGTGT 3100
CGTCTTCCCGGGAGTTTACGAAGAGGCAAAGGAACTGATAGAAGAGGACA
GAGTAGTGGTAGTCAAAGGTTTTCTGGACGAGGACCTTGAAACGGAAAAT 3200
GTCAAGTTCGTGGTGAAAGAGGTTTTCTCCCCTGAGGAGTTCGCAAAGGA
GATGAGGAATACCCTTTATATATTCTTAAAAAGAGAGCAAGCCCTAAACG 3300
GCGTTGCCGAAAAACTAAAGGGAATTATTGAAAACAACAGGACGGAGGAC
GGATACAACTTGGTTCTCACGGTTGATCTGGGAGACTACTTCGTTGATTT 3400
AGCACTCCCACAAGATATGAAACTAAAGGCTGACAGAAAGGTTGTAGAGG
AGATAGAAAAACTGGGAGTGAAGGTCATAATTTAGTAAATAACCCTTACT 3500
TCCGAGTAGTCCCC

FIG. 34B

```
MSKDFVHLHLHTQFSLLDGAIKIDELVKKAKEYGYKAVGMSDHGNLFGSY
KFYKALKAEGIKPIIGMEAYFTTGSRFDRKTKTSEDNITDKYNHHLILIA   100
KDDKGLKNLMKLSTLAYKEGFYYKPRIDYELLEKYGEGLIALTACLKGVP
TYYASINEVKKAEEWVKKFKDIFGDDLYLELQANNIPEQEVANRNLIEIA   200
KKYDVKLIATQDAHYLNPEDRYAHTVLMALQMKKTIHELSSGNFKCSNED
LHFAPPEYMWKKFEGKFEGWEKALLNTLEVMEKTADSFEIFENSTYLLPK   300
YDVPPDKTLEEYLRELAYKGLRQRIERGQAKDTKEYWERLEYELEVINKM
GFAGYFLIVQDFINWAKKNDIPVGPGRGSAGGSLVAYAIGITDVDPIKHG   400
FLFERFLNPERVSMPDIDVDFCQDNREKVIEYVRNKYGHDNVAQIITYNV
MKAKQTLRDVARAMGLPYSTADKLAKLIPQGDVQGTWLSLEEMYKTPVEE   500
LLQKYGEHRTDIEDNVKKFRQICEESPEIKQLVETALKLEGLTRHTSLHA
AGVVIAPKPLSELVPLYYDKEGEVATQYDMVQLEELGLLKMDFLGLKTLT   600
ELKLMKELIKERHGVDINFLELPLDDPKVYKLLQEGKTTGVFQLESRGMK
ELLKKLKPDSFDDIVAVLALYRPGPLKSGLVDTYIKRKHGKEPVEYPFPE   700
LEPVLKETYGVIVYQEQVMKMSQILSGFTPGEADTLRKAIGKKKADLMAQ
MKDKFIQGAVERGYPEEKIRKLWEDIEKFASYSFNKSHSVAYGYISYWTA   800
YVKAHYPAEFFAVKLTTEKNDNKFLNLIKDAKLFGFEILPPDINKSDVGF
TIEGENRIRFGLARIKGVGEETAKIIVEARKKYKQFKGLADFINKTKNRK   900
INKKVVEALVKAGAFDFTKKKRKELLAKVANSEKALMATQNSLFGAPKEE
VEELDPLKLEKEVLGFYISGHPLDNYEKLLKNRYTPIEDLEEWDKESEAV  1000
LTGVITELKVKKTKNGDYMAVFNLVDKTGLIECVVFPGVYEEAKELIEED
RVVVVKGFLDEDLETENVKFVVKEVFSPEEFAKEMRNTLYIFLKREQALN  1100
GVAEKLKGIIENNRTEDGYNLVLTVDLGDYFVDLALPQDMKLKADRKVVE
EIEKLGVKVII                                          1161
```

FIG. 35

ATGAACTACGTTCCCTTCGCGAGAAAGTACAGACCGAAATTCTTCAGGGA
AGTAATAGGACAGGAAGCTCCCGTAAGGATACTCAAAAACGCTATAAAAA 100
ACGACAGAGTGGCTCACGCCTACCTCTTTGCCGGACCGAGGGGGGTTGGG
AAGACGACTATTGCAAGAATTCTCGCAAAAGCTTTGAACTGTAAAAATCC 200
CTCCAAAGGTGAGCCCTGCGGTGAGTGCGAAAACTGCAGGGAGATAGACA
GGGGTGTGTTCCCTGACTTAATTGAAATGGATGCCGCCTCAAACAGGGGT 300
ATAGACGACGTAAGGGCATTAAAAGAAGCGGTCAATTACAAACCTATAAA
AGGAAAGTACAAGGTTTACATAATAGACGAAGCTCACATGCTCACGAAAG 400
AAGCTTTCAACGCTCTCTTAAAAACCCTCGAAGAGCCCCCTCCCAGAACT
GTTTTCGTCCTTTGTACCACGGAGTACGACAAAATTCTTCCCACGATACT 500
CTCAAGGTGTCAGAGGATAATCTTCTCAAAGGTAAGAAAGGAAAAAGTAA
TAGAGTATCTAAAAAAGATATGTGAAAAGGAAGGGATTGAGTGCGAAGAG 600
GGAGCCCTTGAGGTTCTGGCTCATGCCTCTGAAGGGTGCATGAGGGATGC
AGCCTCTCTCCTGGACCAGGCGAGCGTTTACGGGGAAGGCAGGGTAACAA 700
AAGAAGTAGTGGAGAACTTCCTCGGAATTCTCAGTCAGGAAAGCGTTAGG
AGTTTTCTGAAATTGCTTCTGAACTCAGAAGTGGACGAAGCTATAAAGTT 800
CCTCAGAGAACTCTCAGAAAAGGGCTACAACCTGACCAAGTTTTGGGAGA
TGTTAGAAGAGGAAGTGAGAAACGCAATTTTAGTAAAGAGCCTGAAAAAT 900
CCCGAAAGCGTGGTTCAGAACTGGCAGGATTACGAAGACTTCAAAGACTA
CCCTCTGGAAGCCCTCCTCTACGTTGAGAACCTGATAAACAGGGGTAAAG 1000
TTGAAGCGAGAACGAGAGAACCCTTAAGAGCCTTTGAACTCGCGGTAATA
AAGAGCCTTATAGTCAAAGACATAATTCCCGTATCCCAGCTCGGAAGTGT 1100
GGTAAAGGAAACCAAAAAGGAAGAAAAGAAAGTTGAAGTAAAAGAAGAGC
CAAAAGTAAAAGAAGAAAAACCAAAGGAGCAGGAAGAGGACAGGTTCCAG 1200
AAAGTTTTAAACGCTGTGGACGGCAAAATCCTTAAAAGAATACTTGAAGG
GGCAAAAAGGGAAGAAAGAGACGGAAAAATCGTCCTAAAGATAGAAGCCT 1300
CTTATCTGAGAACCATGAAAAAGGAATTTGACTCACTAAAGGAGACTTTT
CCTTTTTTAGAGTTTGAACCCGTGGAGGATAAAAAAAAACCTCAGAAGTC 1400
CAGCGGGACGAGGCTGTTTTAAAGGTAAAGGAGCTCTTCAATGCAAAAAT
ACTCAAAGTACGAAGTAAAAGCTAAGGTCATAAAGGTGAGAATGCCCGTG 1500
GAAGAGATAGGGCTGTTTAACGCACTAATAGACGGCTTGCCCAGGTACGC
ACTCACGAGGACGAAGGAAAAGGGAAAGGGAGAAGTTTTCGTTTTAGCGA 1600
CTCCTTATAAAGTCAAGGAATTGATGGAAGCTATGGAGGGTATGAAAAAA
CACATAAAGGATTTAGAAATCCTCGGAGAGACGGATGAGGATTTAACTTT 1700
TTAAAGTATGGGTGTATCTGAGCAAAGGTTTAAGCTAAAAACAAACCTGA
AACCCGCAGGGGACCAGCCGAAAGCCATAAAAAAACTCCTTGAAAACCTA 1800
AGGAAAGGCGTAAAAGAACAAACACTTCTCGGAGTCACGGGAAGCGGAAA
GACTTTTACTCTAGCAAACGTAATAGCGAAGTACAACAAACCAACTCTTG 1900
TGGTAGTTCACAACAAAATTCTCGCGGCACAGCTATACAGGGAGTTTAAA
GAACTATTCCCTGAAAACGCTGTAGAGTACTTTGTCTCTTACTACGACTA 2000
TTACCAACCTGAAGCCTACATTCCCGAAAAAGATTTATACATAGAAAAGG
ACGCGAGTATAAACGAAAGCTGGAACGTTTCAGACACTCCGCCACGATAT 2100
CCGTTCTAGAAAGGAGGGACGTTATAGTAGTTGCTTCAGTTTCTTGCATA
TACGGACTCGGGAAACCTGAGCACTACGAAAACCTGAGGATAAAACTCCA 2200
AAGGGGAATAAGACTGAACTTGAGTAAGCTCCTGAGGAAACTCGTTGAGC
TAGGATATCAGAGAAATGACTTTGCCATAAAGAGGGCTACCTTCTCGGTT 2300
AGGGGAGACGTGGTTGAGATAGTCCCTTCTCACACGGAAGATTACCTCGT
GAGGGTAGAGTTCTGGGACGACGAAGTTGAAAGAATAGTCCTCATGGACG 2400
CTCTGAAC

FIG. 36

```
MNYVPFARKYRPKFFREVIGQEAPVRILKNAIKNDRVAHAYLFAGPRGVG
KTTIARILAKALNCKNPSKGEPCGECENCREIDRGVFPDLIEMDAASNRG    100
IDDVRALKEAVNYKPIKGKYKVYIIDEAHMLTKEAFNALLKTLEEPPPRT
VFVLCTTEYDKILPTILSRCQRIIFSKVRKEKVIEYLKKICEKEGIECEE    200
GALEVLAHASEGCMRDAASLLDQASVYGEGRVTKEVVENFLGILSQESVR
SFLKLLLNSEVDEAIKFLRELSEKGYNLTKFWEMLEEEVRNAILVKSLKN    300
PESVVQNWQDYEDFKDYPLEALLYVENLINRGKVEARTREPLRAFELAVI
KSLIVKDIIPVSQLGSVVKETKKEEKKVEVKEEPKVKEEKPKEQEEDRFQ    400
KVLNAVDGKILKRILEGAKREERDGKIVLKIEASYLRTMKKEFDSLKETF
PFLEFEPVEDKKKPQKSSGTRLF                                473
```

FIG. 37

```
ATGCGCGTTAAGGTGGACAGGGAGGAGCTTGAAGAGGTTCTTAAAAAAGC
AAGAGAAAGCACGGAAAAAAAAGCCGCACTCCCGATACTCGCGAACTTCT    100
TACTCTCCGCAAAAGAGGAAAACTTAATCGTAAGGGCAACGGACTTGGAA
AACTACCTTGTAGTCTCCGTAAAGGGGGAGGTTGAAGAGGAAGGAGAGGT    200
TTGCGTCCACTCTCAAAAACTCTACGATATAGTCAAGAACTTAAATTCCG
CTTACGTTTACCTTCATACGGAAGGTGAAAAACTCGTCATAACGGGAGGA    300
AAGAGTACGTACAAACTTCCGACAGCTCCCGCGGAGGACTTTCCCGAATT
TCCAGAAATCGTAGAAGGAGGAGAAACACTTTCGGGAAACCTTCTCGTTA    400
ACGGAATAGAAAAGGTAGAGTACGCCATAGCGAAGGAAGAAGCGAACATA
GCCCTTCAGGGAATGTATCTGAGAGGATACGAGGACAGAATTCACTTTGT    500
GTTCGGACGGTCACAGGCTTGCACTTTATGAACCTCTACGTAAACATTGA
AAAGAGTGAAGACGAGTCTTTTGCTTACTTCTCCACTCCCGAGTGGAAAC    600
TCGCCGTTAGCTCCTGGAAGGAGAATTCCCGGACTACATGAGTGTCATCC
CTGAGGAGTTTTCGGCGGAAGTCTTGTTTGAGACAGAGGAAGTCTTAAAG    700
GTTTTAAAGAGGTTGAAGGCTTTAAGCGAAGGAAAAGTTTTTCCCGTGAA
GATTACCTTAAGCGAAAACCTTGCCATCTTTGAGTTCGCGGATCCGGAGT    800
TCGGAGAAGCGAGAGAGGAAATTGAAGTGGAGTACACGGGAGAGCCCTTT
GAGATAGGATTCAACGGAAATACCTTATGGAGGCGCTTGACGCCTACGAC    900
AGCGAAAGAGTGTGGTTCAAGTTCACAACCCCCGACACGGCCACTTTATT
GGAGGCTGAAGATTACGAAAAGGAACCTTACAAGTGCATAATAATGCCGA   1000
TGAGGGTGTAGCCATGAAAAAAGCTTTAATCTTTTTATTGAGCTTGAGCC
TTTTAATTCCTGCGTTTAGCGAAGCCAAACCCAAGTCTTC             1090
```

FIG. 38

```
MRVKVDREELEEVLKKARESTEKKAALPILANFLLSAKEENLIVRATDLE
NYLVVSVKGEVEEEGEVCVHSQKLYDIVKNLNSAYVYLHTEGEKLVITGG    100
KSTYKLPTAPAEDFPEFPEIVEGGETLSGNLLVNGIEKVEYAIAKEEANI
ALQGMYLRGYEDRIHFVGSDGHRLALYEPLGEFSKELLIPRKSLKVLKKL    200
ITGIEDVNIEKSEDESFAYFSTPEWKLAVRLLEGEFPDYMSVIPEEFSAE
VLFETEEVLKVLKRLKALSEGKVFPVKITLSENLAIFEFADPEFGEAREE    300
IEVEYTGEPFEIGFNGKYLMEALDAYDSERVWFKFTTPDTATLLEAEDYE
KEPYKCIIMPMRV                                          363
```

FIG. 39

```
GTGGAAACCACAATATTCCAGTTCCAGAAAACTTTTTTCACAAAACCTCC
GAAGGAGAGGGTCTTCGTCCTTCATGGAGAAGAGCAGTATCTCATAAGAA    100
CCTTTTTGTCTAAGCTGAAGGAAAAGTACGGGGAGAATTACACGGTTCTG
TGGGGGGATGAGATAAGCGAGGAGGAATTCTACACTGCCCTTTCCGAGAC    200
CAGTATATTCGGCGGTTCAAAGGAAAAAGCGGTGGTCATTTACAACTTCG
GGGATTTCCTGAAGAAGCTCGGAAGGAAGAAAAAGGAAAAAGAAAGGCTT    300
ATAAAAGTCCTCAGAAACGTAAAGAGTAACTACGTATTTATAGTGTACGA
TGCGAAACTCCAGAAACAGGAACTTTCTTCGGAACCTCTGAAATCCGTAG    400
CGTCTTTCGGCGGTATAGTGGTAGCAAACAGGCTGAGCAAGGAGAGGATA
AAACAGCTCGTCCTTAAGAAGTTCAAAGAAAAAGGGATAAACGTAGAAAA    500
CGATGCCCTTGAATACCTTCTCCAGCTCACGGGTTACAACTTGATGGAGC
TCAAACTTGAGGTTGAAAAACTGATAGATTACGCAAGTGAAAAGAAAATT    600
TTAACACTCGATGAGGTAAAGAGAGTAGCCTTCTCAGTCTCAGAAAACGT
AAACGTATTTGAGTTCGTTGATTTACTCCTCTTAAAAGATTACGAAAAGG    700
CTCTTAAAGTTTTGGACTCCCTCATTTCCTTCGGAATACACCCCCTCCAG
ATTATGAAAATCCTGTCCTCCTATGCTCTAAAACTTTACACCCTCAAGAG    800
GCTTGAAGAGAAGGGAGAGGACCTGAATAAGGCGATGGAAAGCGTGGGAA
TAAAGAACAACTTTCTCAAGATGAAGTTCAAATCTTACTTAAAGGCAAAC    900
TCTAAAGAGGACTTGAAGAACCTAATCCTCTCCCTCCAGAGGATAGACGC
TTTTTCTAAACTTTACTTTCAGGACACAGTGCAGTTGCTGGGGATTTCTT   1000
GACCTCAAGACTGGAGAGGGAAGTTGTGAAAAATACTTCTCATGGTGGAT
AATCTTTTTTATGAAGTTTGCGGTTTGCGTTTTTCCCGGTTCT          1093
```

FIG. 40

```
VETTIFQFQKTFFTKPPKERVFVLHGEEQYLIRTFLSKLKEKYGENYTVL
WGDEISEEEFYTALSETSIFGGSKEKAVVIYNFGDFLKKLGRKKKEKERL    100
IKVLRNVKSNYVFIVYDAKLQKQELSSEPLKSVASFGGIVVANRLSKERI
KQLVLKKFKEKGINVENDALEYLLQLTGYNLMELKLEVEKLIDYASEKKI    200
LTLDEVKRVAFSVSENVNVFEFVDLLLLKDYEKALKVLDSLISFGIHPLQ
IMKILSSYALKLYTLKRLEEKGEDLNKAMESVGIKNNFLKMKFKSYLKAN    300
SKEDLKNLILSLQRIDAFSKLYFQDTVQLLRDFLTSRLEREVVKNTSHGG
```

FIG. 41

```
ATGGAAAAAGTTTTTTTGGAAAAACTCCAGAAAACCTTGCACATACCCGG
AGGACTCCTTTTTTACGGCAAAGAAGGAAGCGGAAAGACGAAAACAGCTT    100
TTGAATTTGCAAAAGGTATTTTATGTAAGGAAAACGTACCTGGGGATGCG
GAAGTTGTCCCTCCTGCAAACACGTAAACGAGCTGGAGGAAGCCTTCTTT    200
AAAGGAGAAATAGAAGACTTTAAAGTTTATAAGACAAGGACGGTAAAAAG
CACTTCGTTTACCTTATGGGCGAACATCCCGACTTTGTGGTAATAATCCC    300
GAGCGGACATTACATAAAGATAGAACAGATAAGGGAAGTTAAGAACTTTG
CCTATGTGAAGCCCGCACTAAGCAGGAGAAAAGTAATTATAATAGACGAC    400
GCCCACGCGATGACCTCTCAGGCGGCAAACGCTCTTTTAAAGGTATTGGA
AGAGCCACCTGCGGACACCACCTTTATCTTGACCACGAACAGGCGTTCTG    500
CAATCCTGCCGACTATCCTCTCCAGAACTTTTCAAGTGGAGTTCAAGGGC
TTTTCAGTAAAAGAGGTTATGGAAATAGCGAAAGTAGACGAGGAAATAGC    600
GAAACTCTCTGGAGGCAGTCTAAAAAGGGCTATCTTACTAAAGGAAAACA
AAGATATCCTAAACAAAGTAAAGGAATTCTTGGAAAACGAGCCGTTAAAA    700
GTTTACAAGCTTGCAAGTGAATTCGAAAAGTGGGAACCTGAAAAGCAAAA
ACTCTTCCTTGAAATTATGGAAGAATTGGTATCTCAAAAATTGACCGAAG    800
AGAAAAAAGACAATTACACCTACCTTCTTGATACGATCAGACTCTTTAAA
GACGGACTCGCAAGGGGTGTAAACGAACCTCTGTGGCTGTTTACGTTAGC    900
CGTTCAGGCGGATTAATAAACCGTTATTGATTCCGTAACATTTAAACCTT
AATCTAAATTATGAGAGCCTTTGAAGGAGGTCTGGTATGGAAAATTTGAA   1000
GATTAGATATATAGATACGAGGAAGATAGGAACCGTGAGCGGTGTAAAAG
T                                                     1051
```

FIG. 42

```
MEKVFLEKLQKTLHIPGGLLFYGKEGSGKTKTAFEFAKGILCKENVPWGC
GSCPSCKHVNELEEAFFKGEIEDFKVYKDKDGKKHFVYLMGEHPDFVVII    100
PSGHYIKIEQIREVKNFAYVKPALSRRKVIIIDDAHAMTSQAANALLKVL
EEPPADTTFILTTNRRSAILPTILSRTFQVEFKGFSVKEVMEIAKVDEEI    200
AKLSGGSLKRAILLKENKDILNKVKEFLENEPLKVYKLASEFEKWEPEKQ
KLFLEIMEELVSQKLTEEKKDNYTYLLDTIRLFKDGLARGVNEPLWLFTL    300
AVQAD
```

FIG. 43

```
ATGAACTTCCTGAAAAAGTTCCTTTTACTGAGAAAAGCTCAAAAGTCTCC
TTACTTCGAAGAGTTCTACGAAGAAATCGATTTGAACCAGAAGGTGAAAG    100
ATGCAAGGTTTGTAGTTTTTGACTGCGAAGCCACAGAACTCGACGTAAAG
AAGGCAAAACTCCTTTCAATAGGTGCGGTTGAGGTTAAAAACCTGGAAAT    200
AGACCTCTCTAAATCTTTTTACGAGATACTCAAAAGTGACGAGATAAAGG
CGGCGGAGATACATGGAATAACCAGGGAAGACGTTGAAAAGTACGGAAAG    300
GAACCAAAGGAAGTAATATACGACTTTCTGAAGTACATAAAGGGAAGCGT
TCTCGTTGGCTACTACGTGAAGTTTGACGTCTCACTCGTTGAGAAGTACT    400
CCATAAAGTACTTCCAGTATCCAATCATCAACTACAAGTTAGACCTGTTT
AGTTTCGTGAAGAGAGAGTACCAGAGTGGCAGGAGTCTTGACGACCTTAT    500
GAAGGAACTCGGTGTAGAAATAAGGGCAAGGCACAACGCCCTTGAAGATG
CCTACATAACCGCTCTTCTTTTCCTAAAGTACGTTTACCCGAACAGGGAG    600
TACAGACTAAAGGATCTCCCGATTTTCCTT
```

FIG. 44

```
MNFLKKFLLLRKAQKSPYFEEFYEEIDLNQKVKDARFVVFDCEATELDVK
KAKLLSIGAVEVKNLEIDLSKSFYEILKSDEIKAAEIHGITREDVEKYGK    100
EPKEVIYDFLKYIKGSVLVGYYVKFDVSLVEKYSIKYFQYPIINYKLDLF
SFVKREYQSGRSLDDLMKELGVEIRARHNALEDAYITALLFLKYVYPNRE    200
YRLKDLPIFL
```

FIG. 45

```
ATGCTCAATAAGGTTTTTATAATAGGAAGACTTACGGGTGACCCCGTTAT
AACTTATCTACCGAGCGGAACGCCCGTAGTAGAGTTTACTCTGGCTTACA    100
ACAGAAGGTATAAAAACCAGAACGGTGAATTTCAGGAGGAAAGTCACTTC
TTTGACGTAAAGGCGTACGGAAAAATGGCTGAAGACTGGGCTACACGCTT    200
CTCGAAAGGATACCTCGTACTCGTAGAGGGAAGACTCTCCCAGGAAAAGT
GGGAGAAAGAAGGAAAGAAGTTCTCAAAGGTCAGGATAATAGCGGAAAAC    300
GTAAGATTAATAAACAGGCCGAAAGGTGCTGAACTTCAAGCAGAAGAAGA
GGAGGAAGTTCCTCCCATTGAGGAGGAAATTGAAAAACTCGGTAAAGAGG    400
AAGAGAAGCCTTTTACCGATGAAGAGGACGAAATACCTTTTTAATTTTGA
GGAGGTTAAAGTATGGTAGTGAGAGCTCCTAAGAAGAAAGTTTGTATGTA    500
CTGTGAACAAAAGAGAGAGCCAGATT
```

FIG. 46

```
MLNKVFIIGRLTGDPVITYLPSGTPVVEFTLAYNRRYKNQNGEFQEESHF
FDVKAYGKMAEDWATRFSKGYLVLVEGRLSQEKWEKEGKKFSKVRIIAEN    100
VRLINRPKGAELQAEEEEEVPPIEEEIEKLGKEEEKPFTDEEDEIPF
```

FIG. 47

```
ATGCAATTTGTGGATAAACTTCCCTGTGACGAATCCGCCGAGAGGGCGGT
TCTTGGCAGTATGCTTGAAGACCCCGAAAACATACCTCTGGTACTTGAAT    100
ACCTTAAAGAAGAAGACTTCTGCATAGACGAGCACAAGCTACTTTTCAGG
GTTCTTACAAACCTCTGGTCCGAGTACGGCAATAAGCTCGATTTCGTATT    200
AATAAAGGATCACCTTGAAAAGAAAAACTTACTCCAGAAAATACCTATAG
ACTGGCTCGAAGAACTCTACGAGGAGGCGGTATCCCCTGACACGCTTGAG    300
GAAGTCTGCAAAATAGTAAAACAACGTTCCGCACAGAGGGCGATAATTCA
ACTCGGTATAGAACTCATTCACAAAGGAAAGGAAAACAAAGACTTTCACA    400
CATTAATCGAGGAAGCCCAGAGCAGGATATTTTCCATAGCGGAAAGTGCT
ACATCTACGCAGTTTTACCATGTGAAAGACGTTGCGGAAGAAGTTATAGA    500
ACTCATTTATAAATTCAAAAGCTCTGACAGGCTAGTCACGGGACTCCCAA
GCGGTTTCACGGAACTCGATCTAAAGACGACGGGATTCCACCCTGGAGAC    600
TTAATAATACTCGCCGCAAGACCCGGTATGGGGAAAACCGCCTTTATGCT
CTCCATAATCTACAATCTCGCAAAAGACGAGGGAAAACCCTCAGCTGTAT    700
TTTCCTTGGAAATGAGCAAGGAACAGCTCGTTATGAGACTCCTCTCTATG
ATGTCGGAGGTCCCACTTTTCAAGATAAGGTCTGGAAGTATATCGAATGA    800
AGATTTAAAGAAGCTTGAAGCAAGCGCAATAGAACTCGCAAAGTACGACA
TATACCTCGACGACACACCCGCTCTCACTACAACGGATTTAAGGATAAGG    900
GCAAGAAAGCTCAGAAAGGAAAAGGAAGTTGAGTTCGTGGCGGTGGACTA
CTTGCAACTTCTGAGACCGCCAGTCCGAAAGAGTTCAAGACAGGAGGAAG   1000
TGGCAGAGGTTTCAAGAAACTTAAAAGCCCTTGCAAAGGAACTTCACATT
CCCGTTATGGCACTTGCGCAGCTCTCCCGTGAGGTGGAAAAGAGGAGTGA   1100
TAAAAGACCCCAGCTTGCGGACCTCAGAGAATCCGGACAGATAGAACAGG
ACGCAGACCTAATCCTTTTCCTCCACAGACCCGAGTACTACAAGAAAAAG   1200
CCAAATCCCGAAGAGCAGGGTATAGCGGAAGTGATAATAGCCAAGCAAAG
GCAAGGACCCACGGACATTGTGAAGCTCGCATTTATTAAGGAGTACACTA   1300
AGTTTGCAAACCTAGAAGCCCTTCCTGAACAACCTCCTGAAGAAGAGGAA
CTTTCCGAAATTATTGAAACACAGGAGGATGAAGGATTCGAAGATATTGA   1400
CTTCTGAAAATTAAGGTTTTATAATTTTATCTTGGCTATCCGGGGTAGCT
CAATCGGCAGAGCGGGTGGCTG                                1472
```

FIG. 48

```
MQFVDKLPCDESAERAVLGSMLEDPENIPLVLEYLKEEDFCIDEHKLLFR
VLTNLWSEYGNKLDFVLIKDHLEKKNLLQKIPIDWLEELYEEAVSPDTLE   100
EVCKIVKQRSAQRAIIQLGITSTQFYHVKDVAEEVIELIYKFKSSDRLVT
GLPSGFTELDLKTTGFHPGDLIILAARPGMGKTAFMLSIIYNLAKDEGKP   200
SAVFSLEMSKEQLVMRLLSMMSEVPLFKIRSGSISNEDLKKLEASAIELA
KYDIYLDDTPALTTTDLRIRARKLRKEKEVEFVAVDYLQLLRPPVRKSSR   300
QEEVAEVSRNLKALAKELHIPVMALAQLSREVEKRSDKRPQLADLRESGQ
IEQDADLILFLHRPEYYKKKPNPEEQGIAEVIIAKQRQGPTDIVKLAFIK   400
EYTKFANLEALPEQPPEEEELSEIIETQEDEGFEDIDF
```

FIG. 49

```
ATGTCCTCGGACATAGACGAACTTAGACGGGAAATAGATATAGTAGACGT
CATTTCCGAATACTTAAACTTAGAGAAGGTAGGTTCCAATTACAGAACGA    100
ACTGTCCCTTTCACCCTGACGATACACCCTCCTTTTACGTGTCTCCAAGT
AAACAAATATTCAAGTGTTTCGGTTGCGGGGTAGGGGGAGACGCGATAAA    200
GTTCGTTTCCCTTTACGAGGACATCTCCTATTTTGAAGCCGCCCTTGAAC
TCGCAAAACGCTACGGAAAGAAATTAGACCTTGAAAAGATATCAAAAGAC    300
GAAAAGGTATACGTGGCTCTTGACAGGGTTTGTGATTTCTACAGGGAAAG
CCTTCTCAAAAACAGAGAGGCAAGTGAGTACGTAAAGAGTAGGGGAATAG    400
ACCCTAAAGTAGCGAGGAAGTTTGATCTTGGGTACGCACCTTCCAGTGAA
GCACTCGTAAAAGTCTTAAAAGAGAACGATCTTTTAGAGGCTTACCTTGA    500
AACTAAAAACCTCCTTTCTCCTACGAAGGGTGTTTACAGGGATCTCTTTC
TTCGGCGTGTCGTGATCCCGATAAAGGATCCGAGGGGAAGAGTTATAGGT    600
TTCGGTGGAAGGAGGATAGTAGAGGACAAATCTCCCAAGTACATAAACTC
TCCAGACAGCAGGGTATTTAAAAAGGGGGAGAACTTATTCGGTCTTTACG    700
AGGCAAAGGAGTATATAAAGGAAGAAGGATTTGCGATACTTGTGGAAGGG
TACTTTGACCTTTTGAGACTTTTTTCCGAGGGAATAAGGAACGTTGTTGC    800
ACCCCTCGGTACAGCCCTGACCCAAAATCAGGCAAACCTCCTTTCCAAGT
TCACAAAAAAGGTCTACATCCTTTACGACGGAGATGATGCGGGAAGAAAG    900
GCTATGAAAAGTGCCATTCCCCTACTCCTCAGTGCAGGAGTGGAAGTTTA
TCCCGTTTACCTCCCCGAAGGATACGATCCCGACGAGTTTATAAAGGAAT   1000
TCGGGAAAGAGGAATTAAGAAGACTGATAAACAGCTCAGGGGAGCTCTTT
GAAACGCTCATAAAAACCGCAAGGGAAAACTTAGAGGAGAAAACGCGTGA   1100
GTTCAGGTATTATCTGGGCTTTATTTCCGATGGAGTAAGGCGCTTTGCTC
TGGCTTCGGAGTTTCACACCAAGTACAAAGTTCCTATGGAAATTTTATTA   1200
ATGAAAATTGAAAAAAATTCTCAAGAAAAAGAAATTAAACTCTCCTTTAA
GGAAAAAATCTTCCTGAAAGGACTGATAGAATTAAAACCAAAAATAGACC   1300
TTGAAGTCCTGAACTTAAGTCCTGAGTTAAAGGAACTCGCAGTTAACGCC
TTAAACGGAGAGGAGCATTTACTTCCAAAAGAAGTTCTCGAGTACCAGGT   1400
GGATAACTTGGAGAAACTTTTTAACAACATCCTTAGGGATTTACAAAAAT
CTGGGAAAAAGAGGAAGAAAAGAGGGTTGAAAAATGTAAATACTTAATTA   1500
ACTTTAATAAATTTTTAGAGTTAGGA
```

FIG. 50

```
MSSDIDELRREIDIVDVISEYLNLEKVGSNYRTNCPFHPDDTPSFYVSPS
KQIFKCFGCGVGGDAIKFVSLYEDISYFEAALELAKRYGKKLDLEKISKD    100
EKVYVALDRVCDFYRESLLKNREASEYVKSRGIDPKVARKFDLGYAPSSE
ALVKVLKENDLLEAYLETKNLLSPTKGVYRDLFLRRVVIPIKDPRGRVIG    200
FGGRRIVEDKSPKYINSPDSRVFKKGENLFGLYEAKEYIKEEGFAILVEG
YFDLLRLFSEGIRNVVAPLGTALTQNQANLLSKFTKKVYILYDGDDAGRK    300
AMKSAIPLLLSAGVEVYPVYLPEGYDPDEFIKEFGKEELRRLINSSGELF
ETLIKTARENLEEKTREFRYYLGFISDGVRRFALASEFHTKYKVPMEILL    400
MKIEKNSQEKEIKLSFKEKIFLKGLIELKPKIDLEVLNLSPELKELAVNA
LNGEEHLLPKEVLEYQVDNLEKLFNNILRDLQKSGKKRKKRGLKNVNT     498
```

FIG. 51

```
ATGCAAGATACCGCTACCTGCAGTATTTGTCAGGGGACGGGATTCGTAAA
GACCGAAGACAACAAGGTAAGGCTCTGCGAATGCAGGTTCAAGAAAAGGG    100
ATGTAAACAGGGAACTAAACATCCCAAAGAGGTACTGGAACGCCAACTTA
GACACTTACCACCCCAAGAACGTATCCCAGAACAGGGCACTTTTGACGAT    200
AAGGGTCTTCGTCCACAACTTCAATCCCGAGGAAGGGAAAGGGCTTACCT
TTGTAGGATCTCCTGGAGTCGGCAAAACTCACCTTGCGGTTGCAACATTA    300
AAAGCGATTTATGAGAAGAAGGGAATCAGAGGATACTTCTTCGATACGAA
GGATCTAATATTCAGGTTAAAACACTTAATGGACGAGGGAAAGGATACAA    400
AGTTTTTAAAAACTGTCTTAAACTCACCGGTTTTGGTTCTCGACGACCTC
GGTTCTGAGAGGCTCAGTGACTGGCAGAGGGAACTCATCTCTTACATAAT    500
CACTTACAGGTATAACAACCTTAAGAGCACGATAATAACCACGAATTACT
CACTCCAGAGGGAAGAAGAGAGTAGCGTGAGGATAAGTGCGGATCTTGCA    600
AGCAGACTCGGAGAAAACGTAGTTTCAAAAATTTACGAGATGAACGAGTT
GCTCGTTATAAAGGGTTCCGACCTCAGGAAGTCTAAAAAGCTATCAACCC    700
CATCT
```

FIG. 52

```
MQDTATCSICQGTGFVKTEDNKVRLCECRFKKRDVNRELNIPKRYWNANL
DTYHPKNVSQNRALLTIRVFVHNFNPEEGKGLTFVGSPGVGKTHLAVATL    100
KAIYEKKGIRGYFFDTKDLIFRLKHLMDEGKDTKFLKTVLNSPVLVLDDL
GSERLSDWQRELISYIITYRYNNLKSTIITTNYSLQREEESSVRISADLA    200
SRLGENVVSKIYEMNELLVIKGSDLRKSKKLSTPS
```

FIG. 53

```
ATGAAAAAGATTGAAAATTTGAAGTGGAAAAATGTCTCGTTTAAAAGCCT
GGAAATAGATCCCGATGCAGGTGTGGTTCTCGTTTCCGTGGAAAAATTCT   100
CCGAAGAGATAGAAGACCTTGTGCGTTTACTGGAGAAGAAGACGCGGTTT
CGAGTCATCGTGAACGGTGTTCAAAAAAGTAACGGGGATCTAAGGGGAAA   200
GATACTTTCCCTTCTCAACGGTAATGTGCCTTACATAAAAGATGTTGTTT
TCGAAGGAAACAGGCTGATTCTGAAAGTGCTTGGAGATTTCGCGCGGGAC   300
AGGATCGCCTCCAAACTCAGAAGCACGAAAAAACAGCTCGATGAACTGCT
GCCTCCCGGAACAGAGATCATGCTGGAGGTTGTGGAGCCTCCGGAAGATC   400
TTTTGAAAAAGGAAGTACCACAACCAGAAAAGAGAGAAGAACCAAAGGGT
GAAGAATTGAAGATCGAGGATGAAAACCACATCTTTGGACAGAAACCCAG   500
AAAGATCGTCTTCACCCCCTCAAAAATCTTTGAGTACAACAAAAAGACAT
CGGTGAAGGGCAAGATCTTCAAAATAGAGAAGATCGAGGGGAAAAGAACG   600
GTCCTTCTGATTTACCTGACAGACGGAGAAGATTCTCTGATCTGCAAAGT
CTTCAACGACGTTGAAAAGGTCGAAGGGAAAGTATCGGTGGGAGACGTGA   700
TCGTTGCCACAGGAGACCTCCTTCTCGAAAACGGGGAGCCCACCCTTTAC
GTGAAGGGAATCACAAAACTTCCCGAAGCGAAAAGGATGGACAAATCTCC   800
GGTTAAGAGGGTGGAGCTCCACGCCCATACCAAGTTCAGCGATCAGGACG
CAATAACAGATGTGAACGAATATGTGAAACGAGCCAAGGAATGGGGCTTT   900
CCCGCGATAGCCCTCACGGATCATGGGAACGTTCAGGCCATACCTTACTT
CTACGACGCGGCGAAAGAAGCTGGAATAAAGCCCATTTTCGGTATCGAAG  1000
CGTATCTGGTGAGTGACGTGGAGCCCGTCATAAGGAATCTCTCCGACGAT
TCGACGTTTGGAGATGCCACGTTCGTCGTCCTCGACTTCGAGACGACGGG  1100
TCTCGACCCGCAGGTGGATGAGATCATCGAGATAGGAGCGGTGAAGATAC
AGGGTGGCCAGATAGTGGACGAGTACCACACTCTCATAAAGCCTTCCAGG  1200
GAGATCTCAAGAAAAAGTTCGGAGATCACCGGAATCACTCAAGAGATGCT
GGAAAACAAGAGAAGCATCGAGGAAGTTCTGCCGGAGTTCCTCGGTTTTC  1300
TGGAAGATTCCATCATCGTAGCACACAACGCCAACTTCGACTACAGATTT
CTGAGGCTGTGGATCAAAAAAGTGATGGGATTGGACTGGGAAAGACCCTA  1400
CATAGATACGCTCGCCCTCGCAAAGTCCCTTCTCAAACTGAGAAGCTACT
CTCTGGATTCCGTTGTGGAAAAGCTCGGATTGGGTCCCTTCCGGCACCAC  1500
AGGGCCCTGGATGACGCGAGGGTCACCGCTCAGGTTTTCCTCAGGTTCGT
TGAGATGATGAAGAAGATCGGTATCACGAAGCTTTCAGAAATGGAGAAGT  1600
TGAAGGATACGATAGACTACACCGCGTTGAAACCCTTCCACTGCACGATC
CTCGTTCAGAACAAAAAGGGATTGAAAAACCTATACAAACTGGTTTCTGA  1700
TTCCTATATAAAGTACTTCTACGGTGTTCCGAGGATCCTCAAAAGTGAGC
TCATCGAGAACAGAGAAGGACTGCTCGTGGGTAGCGCGTGTATCTCCGGT  1800
GAGCTCGGACGTGCCGCCCTCGAAGGAGCGAGTGATTCAGAACTCGAAGA
GATCGCGAAGTTCTACGACTACATAGAAGTCATGCCGCTCGACGTTATAG  1900
CCGAAGATGAAGAAGACCTAGACAGAGAAAGACTGAAAGAAGTGTACCGA
AAACTCTACAGAATAGCGAAAAAATTGAACAAGTTCGTCGTCATGACCGG  2000
TGATGTTCATTTCCTCGATCCCGAAGATGCCAGGGGCAGAGCTGCACTTC
TGGCACCTCAGGGAAACAGAAACTTCGAGAATCAGCCCGCACTCTACCTC  2100
AGAACGACCGAAGAAATGCTCGAGAAGGCGATAGAGATATTCGAAGATGA
AGAGATCGCGAGGGAAGTCGTGATAGAGAATCCCAACAGAATAGCCGATA  2200
TGATCGAGGAAGTGCAGCCGCTCGAGAAAAAACTTCACCCGCCGATCATA
GAGAACGCCGATGAAATAGTGAGAAACCTCACCATGAAGCGGGCGTACGA  2300
GATCTACGGTGATCCGCTTCCCGAAATCGTCCAGAAGCGTGTGGAAAAGG
```

FIG. 54A

```
AACTGAACGCCATCATAAATCATGGATACGCCGTTCTCTATCTCATCGCT   2400
CAGGAGCTCGTTCAGAAATCTATGAGCGATGGTTACGTGGTTGGATCCAG
AGGATCCGTCGGGTCTTCACTCGTGGCCAATCTCCTCGGAATAACAGAGG   2500
TGAATCCCCTACCACCACATTACAGGTGTCCAGAGTGCAAATACTTTGAA
GTTGTCGAAGACGACAGATACGGAGCGGGTTACGACCTTCCCAACAAGAA   2600
CTGTCCAAGATGTGGGGCTCCTCTCAGAAAAGACGGCCACGGCATACCGT
TTGAAACGTTCATGGGGTTCGAGGGTGACAAGGTCCCCGACATAGATCTC   2700
AACTTCTCAGGAGAGTATCAGGAACGTGCTCATCGTTTTGTGGAAGAACT
CTTCGGTAAAGACCACGTCTATAGGGCGGGAACCATAAACACCATCGCGG   2800
AAAGAAGTGCGGTGGGTTACGTGAGAAGCTACGAAGAGAAAACCGGAAAG
AAGCTCAGAAAGGCGGAAATGGAAAGACTCGTTTCCATGATCACGGGAGT   2900
GAAGAGAACGACGGGTCAGCACCCAGGGGGGCTCATGATCATACCGAAAG
ACAAAGAAGTCTACGATTTCACTCCCATACAGTATCCAGCCAACGATAGA   3000
AACGCAGGTGTGTTCACCACGCACTTCGCATACGAGACGATCCATGATGA
CCTGGTGAAGATAGATGCGCTCGGCCACGATGATCCCACTTTCATCAAGA   3100
TGCTCAAGGACCTCACCGGAATCGATCCCATGACGATTCCCATGGATGAC
CCCGATACGCTCGCCATATTCAGTTCTGTGAAGCCTCTTGGTGTGGATCC   3200
CGTTGAGCTGGAAAGCGATGTGGGAACGTACGGAATTCCGGAGTTCGGAA
CCGAGTTTGTGAGGGGAATGCTCGTTGAAACGAGACCAAAGAGTTTCGCC   3300
GAGCTTGTGAGAATCTCAGGACTGTCACACGGTACGGACGTCTGGTTGAA
CAACGCACGTGATTGGATAAACCTCGGCTACGCCAAGCTCTCCGAGGTTA   3400
TCTCGTGTAGGGACGACATCATGAACTTCCTCATACACAAAGGAATGGAA
CCGTCACTTGCCTTCAAGATCATGGAAAACGTCAGGAAGGGAAAGGGTAT   3500
CACAGAAGAGATGGAGAGCGAGATGAGAAGGCTGAAGGTTCCAGAATGGT
TCATCGAATCCTGTAAAAGGATCAAATATCTCTTCCCGAAAGCTCACGCT   3600
GTGGCTTACGTGAGTATGGCCTTCAGAATTGCTTACTTCAAGGTTCACTA
TCCTCTTCAGTTTTACGCGGCGTACTTCACGATAAAAGGTGATCAGTTCG   3700
ATCCGGTTCTCGTACTCAGGGGAAAAGAAGCCATAAAGAGGCGCTTGAGA
GAACTCAAAGCGATGCCTGCCAAAGACGCCCAGAAGAAAAACGAAGTGAG   3800
TGTTCTGGAGGTTGCCCTGGAAATGATACTGAGAGGTTTTTCCTTCCTAC
CGCCCGACATCTTCAAATCCGACGCGAAGAAATTTCTGATAGAAGGAAAC   3900
TCGCTGAGAATTCCGTTCAACAAACTTCCAGGACTGGGTGACAGCGTTGC
CGAGTCGATAATCAGAGCCAGGGAAGAAAAGCCGTTCACTTCGGTGGAAG   4000
ATCTCATGAAGAGGACCAAGGTCAACAAAAATCACATAGAGCTGATGAAA
AGCCTGGGTGTTCTCGGGGACCTTCCAGAGACGGAACAGTTCACGCTTTT   4100
C
```

FIG. 54B

```
MKKIENLKWKNVSFKSLEIDPDAGVVLVSVEKFSEEIEDLVRLLEKKTRF
RVIVNGVQKSNGDLRGKILSLLNGNVPYIKDVVFEGNRLILKVLGDFARD    100
RIASKLRSTKKQLDELLPPGTEIMLEVVEPPEDLLKKEVPQPEKREEPKG
EELKIEDENHIFGQKPRKIVFTPSKIFEYNKKTSVKGKIFKIEKIEGKRT    200
VLLIYLTDGEDSLICKVFNDVEKVEGKVSVGDVIVATGDLLLENGEPTLY
VKGITKLPEAKRMDKSPVKRVELHAHTKFSDQDAITDVNEYVKRAKEWGF    300
PAIALTDHGNVQAIPYFYDAAKEAGIKPIFGIEAYLVSDVEPVIRNLSDD
STFGDATFVVLDFETTGLDPQVDEIIEIGAVKIQGGQIVDEYHTLIKPSR    400
EISRKSSEITGITQEMLENKRSIEEVLPEFLGFLEDSIIVAHNANFDYRF
LRLWIKKVMGLDWERPYIDTLALAKSLLKLRSYSLDSVVEKLGLGPFRHH    500
RALDDARVTAQVFLRFVEMMKKIGITKLSEMEKLKDTIDYTALKPFHCTI
LVQNKKGLKNLYKLVSDSYIKYFYGVPRILKSELIENREGLLVGSACISG    600
ELGRAALEGASDSELEEIAKFYDYIEVMPLDVIAEDEEDLDRERLKEVYR
KLYRIAKKLNKFVVMTGDVHFLDPEDARGRAALLAPQGNRNFENQPALYL    700
RTTEEMLEKAIEIFEDEEIAREVVIENPNRIADMIEEVQPLEKKLHPPII
ENADEIVRNLTMKRAYEIYGDPLPEIVQKRVEKELNAIINHGYAVLYLIA    800
QELVQKSMSDGYVVGSRGSVGSSLVANLLGITEVNPLPPHYRCPECKYFE
VVEDDRYGAGYDLPNKNCPRCGAPLRKDGHGIPFETFMGFEGDKVPDIDL    900
NFSGEYQERAHRFVEELFGKDHVYRAGTINTIAERSAVGYVRSYEEKTGK
KLRKAEMERLVSMITGVKRTTGQHPGGLMIIPKDKEVYDFTPIQYPANDR   1000
NAGVFTTHFAYETIHDDLVKIDALGHDDPTFIKMLKDLTGIDPMTIPMDD
PDTLAIFSSVKPLGVDPVELESDVGTYGIPEFGTEFVRGMLVETRPKSFA   1100
ELVRISGLSHGTDVWLNNARDWINLGYAKLSEVISCRDDIMNFLIHKGME
PSLAFKIMENVRKGKGITEEMESEMRRLKVPEWFIESCKRIKYLFPKAHA   1200
VAYVSMAFRIAYFKVHYPLQFYAAYFTIKGDQFDPVLVLRGKEAIKRRLR
ELKAMPAKDAQKKNEVSVLEVALEMILRGFSFLPPDIFKSDAKKFLIEGN   1300
SLRIPFNKLPGLGDSVAESIIRAREEKPFTSVEDLMKRTKVNKNHIELMK
SLGVLGDLPETEQFTLF                                    1367
```

FIG. 55

```
GTGCTCGCCATGATATGGAACGACACCGTTTTTTGCGTCGTAGACACAGA
AACCACGGGAACCGATCCCTTTGCCGGAGACCGGATAGTTGAAATAGCCG    100
CTGTTCCTGTCTTCAAGGGGAAGATCTACAGAAACAAAGCGTTTCACTCT
CTCGTGAATCCCAGAATAAGAATCCCTGCGCTGATTCAGAAAGTTCACGG    200
TATCAGCAACATGGACATCGTGGAAGCGCCAGACATGGACACAGTTTACG
ATCTTTTCAGGGATTACGTGAAGGGAACGGTGCTCGTGTTTCACAACGCC    300
AACTTCGACCTCACTTTTCTGGATATGATGGCAAAGGAAACGGGAAACTT
TCCAATAACGAATCCCTACATCGACACACTCGATCTTTCAGAAGAGATCT    400
TTGGAAGGCCTCATTCTCTCAAATGGCTCTCCGAAAGACTTGGAATAAAA
ACCACGATACGGCACCGTGCTCTTCCAGATGCCCTGGTGACCGCAAGAGT    500
TTTTGTGAAGCTTGTTGAATTTCTTGGTGAAAACAGGGTCAACGAATTCA
TACGTGGAAAACGGGGG                                      567
```

FIG. 56

```
MLAMIWNDTVFCVVDTETTGTDPFAGDRIVEIAAVPVFKGKIYRNKAFHS
LVNPRIRIPALIQKVHGISNMDIVEAPDMDTVYDLFRDYVKGTVLVFHNA    100
NFDLTFLDMMAKETGNFPITNPYIDTLDLSEEIFGRPHSLKWLSERLGIK
TTIRHRALPDALVTARVFVKLVEFLGENRVNEFIRGKRG                189
```

FIG. 57

```
GTGGAAGTTCTTTACAGGAAGTACAGGCCAAAGACTTTTTCTGAGGTTGT
CAATCAGGATCATGTGAAGAAGGCAATAATCGGTGCTATTCAGAAGAACA    100
GCGTGGCCCACGGATACATATTCGCCGGTCCGAGGGGAACGGGGAAGACT
ACTCTTGCCAGAATTCTCGCAAAATCCCTGAACTGTGAGAACAGAAAGGG    200
AGTTGAACCCTGCAATTCCTGCAGAGCCTGCAGAGAGATAGACGAGGGAA
CCTTCATGGACGTGATAGAGCTCGACGCGGCCTCCAACAGAGGAATAGAC    300
GAGATCAGAAGAATCAGAGACGCCGTTGGATACAGGCCGATGGAAGGTAA
ATACAAAGTCTACATAATAGACGAAGTTCACATGCTCACGAAAGAAGCCT    400
TCAACGCGCTCCTCAAAACACTCGAAGAACCTCCTTCCCACGTCGTGTTC
GTGCTGGCAACGACAAACCTTGAGAAGGTTCCTCCCACGATTATCTCGAG    500
ATGTCAGGTTTTCGAGTTCAGAAACATTCCCGACGAGCTCATCGAAAAGA
GGCTCCAGGAAGTTGCGGAGGCTGAAGGAATAGAGATAGACAGGGAAGCT    600
CTGAGCTTCATCGCAAAAAGAGCCTCTGGAGGCTTGAGAGACGCGCTCAC
CATGCTCGAGCAGGTGTGGAAGTTCTCGGAAGGAAAGATAGATCTCGAGA    700
CGGTACACAGGGCGCTCGGGTTGATACCGATACAGGTTGTTCGCGATTAC
GTGAACGCTATCTTTTCTGGTGATGTGAAAAGGGTCTTCACCGTTCTCGA    800
CGACGTCTATTACAGCGGGAAGGACTACGAGGTGCTCATTCAGGAAGCAG
TCGAGGATCTGGTCGAAGACCTGGAAAGGGAGAGAGGGGTTTACCAGGTT    900
TCAGCGAACGATATAGTTCAGGTTTCGAGACAACTTCTGAATCTTCTGAG
AGAGATAAAGTTCGCCGAAGAAAAACGACTCGTCTGTAAAGTGGGTTCGG   1000
CTTACATAGCGACGAGGTTCTCCACCACAAACGTTCAGGAAAACGATGTC
AGAGAAAAAAACGATAATTCAAATGTACAGCAGAAAGAAGAGAAGAAAGA   1100
AACGGTGAAGGCAAAAGAAGAAAAACAGGAAGACAGCGAGTTCGAGAAAC
GCTTCAAAGAACTCATGGAAGAACTGAAAGAAAAGGGCGATCTCTCTATC   1200
TTTGTCGCTCTCAGCCTCTCAGAGGTGCAGTTTGACGGAGAAAAGGTGAT
TATTTCTTTTGATTCATCGAAAGCTATGCATTACGAGTTGATGAAGAAAA   1300
AACTGCCTGAGCTGGAAAACATTTTTTCTAGAAAACTCGGGAAAAAAGTA
GAAGTTGAACTTCGACTGATGGGAAAAGAAGAAACAATCGAGAAGGTTTC   1400
TCAGAAGATCCTGAGATTGTTTGAACAGGAGGGA
```

FIG. 58

```
MEVLYRKYRPKTFSEVVNQDHVKKAIIGAIQKNSVAHGYIFAGPRGTGKT
TLARILAKSLNCENRKGVEPCNSCRACREIDEGTFMDVIELDAASNRGID    100
EIRRIRDAVGYRPMEGKYKVYIIDEVHMLTKEAFNALLKTLEEPPSHVVF
VLATTNLEKVPPTIISRCQVFEFRNIPDELIEKRLQEVAEAEGIEIDREA    200
LSFIAKRASGGLRDALTMLEQVWKFSEGKIDLETVHRALGLIPIQVVRDY
VNAIFSGDVKRVFTVLDDVYYSGKDYEVLIQEAVEDLVEDLERERGVYQV    300
SANDIVQVSRQLLNLLREIKFAEEKRLVCKVGSAYIATRFSTTNVQENDV
REKNDNSNVQQKEEKKETVKAKEEKQEDSEFEKRFKELMEELKEKGDLSI    400
FVALSLSEVQFDGEKVIISFDSSKAMHYELMKKKLPELENIFSRKLGKKV
EVELRLMGKEETIEKVSQKILRLFEQEG                          478
```

FIG. 59

```
ATGAAAGTAACCGTCACGACTCTTGAATTGAAAGACAAAATAACCATCGC
CTCAAAAGCGCTCGCAAAGAAATCCGTGAAACCCATTCTTGCTGGATTTC    100
TTTTCGAAGTGAAAGATGGAAATTTCTACATCTGCGCGACCGATCTCGAG
ACCGGAGTCAAAGCAACCGTGAATGCCGCTGAAATCTCCGGTGAGGCACG    200
TTTTGTGGTACCAGGAGATGTCATTCAGAAGATGGTCAAGGTTCTCCCAG
ATGAGATAACGGAACTTTCTTTAGAGGGGGATGCTCTTGTTATAAGTTCT    300
GGAAGCACCGTTTTCAGGATCACCACCATGCCCGCGGACGAATTTCCAGA
GATAACGCCTGCCGAGTCTGGAATAACCTTCGAAGTTGACACTTCGCTCC    400
TCGAGGAAATGGTTGAAAAGGTCATCTTCGCCGCTGCCAAAGACGAGTTC
ATGCGAAATCTGAATGGAGTTTTCTGGGAACTCCACAAGAATCTTCTCAG    500
GCTGGTTGCAAGTGATGGTTTCAGACTTGCACTTGCTGAAGAGCAGATAG
AAAACGAGGAAGAGGCGAGTTTCTTGCTCTCTTTGAAGAGCATGAAAGAA    600
GTTCAAAACGTGCTGGACAACACAACGGAGCCGACTATAACGGTGAGGTA
CGATGGAAGAAGGGTTTCTCTGTCGACAAATGATGTAGAAACGGTGATGA    700
GAGTGGTCGACGCTGAATTTCCCGATTACAAAAGGGTGATCCCCGAAACT
TTCAAAACGAAAGTGGTGGTTTCCAGAAAAGAACTCAGGGAATCTTTGAA    800
GAGGGTGATGGTGATTGCCAGCAAGGGAAGCGAGTCCGTGAAGTTCGAAA
TAGAAGAAAACGTTATGAGACTTGTGAGCAAGAGCCCGGATTATGGAGAA    900
GTGGTCGATGAAGTTGAAGTTCAAAAAGAAGGGGAAGATCTCGTGATCGC
TTTCAACCCGAAGTTCATCGAGGACGTTTTGAAGCACATTGAGACTGAAG   1000
AAATCGAAATGAACTTCGTTGATTCTACCAGTCCATGTCAGATAAATCCA
CTCGATATTTCTGGATACCTTTACATAGTGATGCCCATCAGACTGGCA     1098
```

FIG. 60

```
MKVTVTTLELKDKITIASKALAKKSVKPILAGFLFEVKDGNFYICATDLE
TGVKATVNAAEISGEARFVVPGDVIQKMVKVLPDEITELSLEGDALVISS    100
GSTVFRITTMPADEFPEITPAESGITFEVDTSLLEEMVEKVIFAAAKDEF
MRNLNGVFWELHKNLLRLVASDGFRLALAEEQIENEEEASFLLSLKSMKE    200
VQNVLDNTTEPTITVRYDGRRVSLSTNDVETVMRVVDAEFPDYKRVIPET
FKTKVVVSRKELRESLKRVMVIASKGSESVKFEIEENVMRLVSKSPDYGE    300
VVDEVEVQKEGEDLVIAFNPKFIEDVLKHIETEEIEMNFVDSTSPCQINP
LDISGYLYIVMPIRLA                                       366
```

FIG. 61

```
ATGCCAGTCACGTTTCTCACAGGTACTGCAGAAACTCAGAAGGAAGAATT
GATAAAGAAACTCCTGAAGGATGGTAACGTGGAGTACATAAGGATCCATC      100
CGGAGGATCCCGACAAGATCGATTTCATAAGGTCTTTACTCAGGACAAAG
ACGATCTTTTCCAACAAGACGATCATTGACATCGTCAATTTCGATGAGTG      200
GAAAGCACAGGAGCAGAAGCGTCTCGTTGAACTTTTGAAAAACGTACCGG
AAGACGTTCATATCTTCATCCGTTCTCAAAAAACAGGTGGAAAGGGAGTA      300
GCGCTGGAGCTTCCGAAGCCATGGGAAACGGACAAGTGGCTTGAGTGGAT
AGAAAAGCGCTTCAGGGAGAATGGTTTGCTCATCGATAAAGATGCCCTTC      400
AGCTGTTTTTCTCCAAGGTTGGAACGAACGACCTGATCATAGAAAGGGAG
ATTGAAAAACTGAAAGCTTATTCCGAGGACAGAAAGATAACGGTAGAAGA      500
CGTGGAAGAGGTCGTTTTTACCTATCAGACTCCGGGATACGATGATTTTT
GCTTTGCTGTTTCCGAAGGAAAAAGGAAGCTCGCTCACTCTCTTCTGTCG      600
CAGCTGTGGAAAACCACAGAGTCCGTGGTGATTGCCACTGTCCTTGCGAA
TCACTTCTTGGATCTCTTCAAAATCCTCGTTCTTGTGACAAAGAAAAGAT      700
ACTACACCTGGCCTGATGTGTCCAGGGTGTCCAAAGAGCTGGGAATTCCC
GTTCCTCGTGTGGCTCGTTTCCTCGGTTTCTCCTTTAAGACCTGGAAATT      800
CAAGGTGATGAACCACCTCCTCTACTACGATGTGAAGAAGGTTAGAAAGA
TACTGAGGGATCTCTACGATCTGGACAGAGCCGTGAAAAGCGAAGAAGAT      900
CCAAAACCGTTCTTCCACGAGTTCATAGAAGAGGTGGCACTGGATGTATA
TTCTCTTCAGAGAGATGAAGAA                                   972
```

FIG. 62

```
MPVTFLTGTAETQKEELIKKLLKDGNVEYIRIHPEDPDKIDFIRSLLRTK
TIFSNKTIIDIVNFDEWKAQEQKRLVELLKNVPEDVHIFIRSQKTGGKGV      100
ALELPKPWETDKWLEWIEKRFRENGLLIDKDALQLFFSKVGTNDLIIERE
IEKLKAYSEDRKITVEDVEEVVFTYQTPGYDDFCFAVSEGKRKLAHSLLS      200
QLWKTTESVVIATVLANHFLDLFKILVLVTKKRYYTWPDVSRVSKELGIP
VPRVARFLGFSFKTWKFKVMNHLLYYDVKKVRKILRDLYDLDRAVKSEED      300
PKPFFHEFIEEVALDVYSLQRDEE
```

FIG. 63

```
ATGAACGATTTGATCAGAAAGTACGCTAAAGATCAACTGGAAACTTTGAA
AAGGATCATAGAAAAGTCTGAAGGAATATCCATCCTCATAAATGGAGAAG    100
ATCTCTCGTATCCGAGAGAAGTATCCCTTGAACTTCCCGAGTACGTGGAG
AAATTTCCCCCGAAGGCCTCGGATGTTCTGGAGATAGATCCCGAGGGGGA    200
GAACATAGGCATAGACGACATCAGAACGATAAAGGACTTCCTGAACTACA
GCCCCGAGCTCTACACGAGAAAGTACGTGATAGTCCACGACTGTGAAAGA    300
ATGACCCAGCAGGCGGCGAACGCGTTTCTGAAGGCCCTTGAAGAACCACC
AGAATACGCTGTGATCGTTCTGAACACTCGCCGCTGGCATTATCTACTGC    400
CGACGATAAAGAGCCGAGTGTTCAGAGTGGTTGTGAACGTTCCAAAGGAG
TTCAGAGATCTCGTGAAAGAGAAAATAGGAGATCTCTGGGAGGAACTTCC    500
ACTTCTTGAGAGAGACTTCAAAACGGCTCTCGAAGCCTACAAACTTGGTG
CGGAAAAACTTTCTGGATTGATGGAAAGTCTCAAAGTTTTGGAGACGGAA    600
AAACTCTTGAAAAAGGTCCTTTCAAAAGGCCTCGAAGGTTATCTCGCATG
TAGGGAGCTCCTGGAGAGATTTTCAAAGGTGGAATCGAAGGAATTCTTTG    700
CGCTTTTTGATCAGGTGACTAACACGATAACAGGAAAAGACGCGTTTCTT
TTGATCCAGAGACTGACAAGAATCATTCTCCACGAAAACACATGGGAAAG    800
CGTTGAAGATCAAAAAAGCGTGTCTTTCCTCGATTCAATTCTCAGGGTGA
AGATAGCGAATCTGAACAACAAACTCACTCTGATGAACATCCTCGCGATA    900
CACAGAGAGAGAAAGAGAGGTGTCAACGCTTGGAGC
```

FIG. 64

```
MNDLIRKYAKDQLETLKRIIEKSEGISILINGEDLSYPREVSLELPEYVE
KFPPKASDVLEIDPEGENIGIDDIRTIKDFLNYSPELYTRKYVIVHDCER    100
MTQQAANAFLKALEEPPEYAVIVLNTRRWHYLLPTIKSRVFRVVVNVPKE
FRDLVKEKIGDLWEELPLLERDFKTALEAYKLGAEKLSGLMESLKVLETE    200
KLLKKVLSKGLEGYLACRELLERFSKVESKEFFALFDQVTNTITGKDAFL
LIQRLTRIILHENTWESVEDKSVSFLDSILRVKIANLNNKLTLMNILAIH    300
RERKRGVNAWS
```

FIG. 65

```
ATGTCTTTCTTCAACAAGATCATACTCATAGGAAGACTCGTGAGAGATCC
CGAAGAGAGATACACGCTCAGCGGAACTCCAGTCACCACCTTCACCATAG    100
CGGTGGACAGGGTTCCCAGAAAGAACGCGCCGGACGACGCTCAAACGACT
GATTTCTTCAGGATCGTCACCTTTGGAAGACTGGCAGAGTTCGCTAGAAC    200
CTATCTCACCAAAGGAAGGCTCGTTCTCGTCGAAGGTGAAATGAGAATGA
GAAGATGGGAAACACCCACTGGAGAAAAGAGGGTATCTCCGGAGGTTGTC    300
GCAAACGTTGTTAGATTCATGGACAGAAAACCTGCTGAAACAGTTAGCGA
GACTGAAGAGGAGCTGGAAATACCGGAAGAAGACTTTTCCAGCGATACCT    400
TCAGTGAAGATGAACCACCATTT
```

FIG. 66

```
MSFFNKIILIGRLVRDPEERYTLSGTPVTTFTIAVDRVPRKNAPDDAQTT
DFFRIVTFGRLAEFARTYLTKGRLVLVEGEMRMRRWETPTGEKRVSPEVV    100
ANVVRFMDRKPAETVSETEEELEIPEEDFSSDTFSEDEPPF
```

FIG. 67

```
ATGCGTGTTCCCCCGCACAACTTAGAGGCCGAAGTTGCTGTGCTCGGAAG
CATATTGATAGATCCGTCGGTAATAAACGACGTTCTTGAAATTTTGAGCC    100
ACGAAGATTTCTATCTGAAAAAACACCAACACATCTTCAGAGCGATGGAA
GAGCTTTACGACGAAGGAAAACCGGTGGACGTGGTTTCCGTCTGTGACAA    200
GCTTCAAAGCATGGGAAAACTCGAGGAAGTAGGTGGAGATCTGGAAGTGG
CCCAGCTCGCTGAGGCTGTGCCCAGTTCTGCACACGCACTTCACTACGCG    300
GAGATCGTCAAGGAAAAATCCATTCTGAGGAAACTCATTGAGATCTCCAG
AAAAATCTCAGAAAGTGCCTACATGGAAGAAGATGTGGAGATCCTGCTCG    400
ACAACGCAGAAAAGATGATCTTCGAGATCTCAGAGATGAAAACGACAAAA
TCCTACGATCATCTGAGAGGCATCATGCACCGGGTGTTTGAAAACCTGGA    500
GAACTTCAGGGAAAGAGCCAACCTTATAGAACCCGGTGTGCTCATAACGG
GACTACCAACGGGATTCAAAAGTCTGGACAAACAGACCACAGGGTTCCAC    600
AGCTCCGATCTGGTGATAATAGCAGCGAGACCCTCCATGGGAAAAACCTC
CTTCGCACTCTCAATAGCGAGGAACATGGCTGTCAATTTCGAAATCCCCG    700
TCGGAATATTCAGTCTCGAGATGTCCAAGGAACAGCTCGCTCAAAGACTA
CTCAGCATGGAGTCCGGTGTGGATCTTTACAGCATCAGAACAGGATACCT    800
GGATCAGGAGAAGTGGGAAAGACTCACAATAGCGGCTTCTAAACTCTACA
AAGCACCCATAGTTGTGGACGATGAGTCACTCCTCGATCCGCGATCGTTG    900
AGGGCAAAAGCGAGAAGGATGAAAAAAGAATACGATGTAAAAGCCATTTT
TGTCGACTATCTCCAGCTCATGCACCTGAAAGGAAGAAAAGAAAGCAGAC   1000
AGCAGGAGATATCCGAGATCTCGAGATCTCTGAAGCTCCTTGCGAGGGAA
CTCGACATAGTGGTGATAGCGCTTTCACAGCTTTCGAGGGCCGTAGAACA   1100
GAGAGAAGACAAAAGACCGAGGCTGAGTGACCTCAGGGAATCCGGTGCGA
TAGAACAGGACGCAGACACAGTCATCTTCATCTACAGGGAGGAATATTAC   1200
AGGAGCAAAAAATCCAAAGAGGAAAGCAAGCTTCACGAACCTCACGAAGC
TGAAATCATAATAGGTAAACAGAGAAACGGTCCCGTTGGAACGATCACTC   1300
TGATCTTCGACCCCAGAACGGTTACGTTCCATGAAGTCGATGTGGTGCAT
TCA                                                   1353
```

FIG. 68

```
MRVPPHNLEAEVAVLGSILIDPSVINDVLEILSHEDFYLKKHQHIFRAME
ELYDEGKPVDVVSVCDKLQSMGKLEEVGGDLEVAQLAEAVPSSAHALHYA   100
EIVKEKSILRKLIEISRKISESAYMEEDVEILLDNAEKMIFEISEMKTTK
SYDHLRGIMHRVFENLENFRERANLIEPGVLITGLPTGFKSLDKQTTGFH   200
SSDLVIIAARPSMGKTSFALSIARNMAVNFEIPVGIFSLEMSKEQLAQRL
LSMESGVDLYSIRTGYLDQEKWERLTIAASKLYKAPIVVDDESLLDPRSL   300
RAKARRMKKEYDVKAIFVDYLQLMHLKGRKESRQQEISEISRSLKLLARE
LDIVVIALSQLSRAVEQREDKRPRLSDLRESGAIEQDADTVIFIYREEYY   400
RSKKSKEESKLHEPHEAEIIIGKQRNGPVGTITLIFDPRTVTFHEVDVVH
S                                                     451
```

FIG. 69

```
GTGATTCCTCGAGAGGTCATCGAGGAAATAAAAGAAAAGGTTGACATCGT
AGAGGTCATTTCCGAGTACGTGAATCTTACCCGGGTAGGTTCCTCCTACA    100
GGGCTCTCTGTCCCTTTCATTCAGAAACCAATCCTTCTTTCTACGTTCAT
CCGGGTTTGAAGATATACCATTGTTTCGGCTGCGGTGCGAGTGGAGACGT    200
CATCAAATTTCTTCAAGAAATGGAAGGGATCAGTTTCCAGGAAGCGCTGG
AAAGACTTGCCAAAAGAGCTGGGATTGATCTTTCTCTCTACAGAACAGAA    300
GGGACTTCTGAATACGGAAAATACATTCGTTTGTACGAAGAAACGTGGAA
AAGGTACGTCAAAGAGCTGGAGAAATCGAAAGAGGCAAAAGACTATTTAA    400
AAAGCAGAGGCTTCTCTGAAGAAGATATAGCAAAGTTCGGCTTTGGGTAC
GTCCCCAAGAGATCCAGCATCTCTATAGAAGTTGCAGAAGGCATGAACAT    500
AACACTGGAAGAACTTGTCAGATACGGTATCGCGCTGAAAAAGGGTGATC
GATTCGTTGATAGATTCGAAGGAAGAATCGTTGTTCCAATAAAGAACGAC    600
AGTGGTCATATTGTGGCTTTTGGTGGGCGTGCTCTCGGCAACGAAGAACC
GAAGTATTTGAACTCTCCAGAGACCAGGTATTTTTCGAAGAAGAAGACCC    700
TTTTTCTCTTCGATGAGGCGAAAAAAGTGGCAAAAGAGGTTGGTTTTTTC
GTCATCACCGAAGGCTACTTCGACGCGCTCGCATTCAGAAAGGATGGAAT    800
ACCAACGGCGGTCGCTGTTCTTGGGGCGAGTCTTTCAAGAGAGGCGATTC
TAAAACTTTCGGCGTATTCGAAAAACGTCATACTGTGTTTCGATAATGAC    900
AAAGCAGGCTTCAGAGCCACTCTCAAATCCCTCGAGGATCTCCTAGACTA
CGAATTCAACGTGCTTGTGGCAACCCCCTCTCCTTACAAAGACCCAGATG   1000
AACTCTTTCAGAAAGAAGGAGAAGGTTCATTGAAAAAGATGCTGAAAAAC
TCGCGTTCGTTCGAATATTTTCTGGTGACGGCTGGTGAGGTCTTCTTTGA   1100
CAGGAACAGCCCCGCGGGTGTGAGATCCTACCTTTCTTTCCTCAAAGGTT
GGGTCCAAAAGATGAGAAGGAAAGGATATTTGAAACACATAGAAAATCTC   1200
GTGAATGAGGTTTCATCTTCTCTCCAGATACCAGAAAACCAGATTTTGAA
CTTTTTTGAAAGCGACAGGTCTAACACTATGCCTGTTCATGAGACCAAGT   1300
CGTCAAAGGTTTACGATGAGGGGAGAGGACTGGCTTATTTGTTTTTGAAC
TACGAGGATTTGAGGGAAAAGATTCTGGAACTGGACTTAGAGGTACTGGA   1400
AGATAAAAACGCGAGGGAGTTTTTCAAGAGAGTCTCACTGGGAGAAGATT
TGAACAAAGTCATAGAAAACTTCCCAAAAGAGCTGAAAGACTGGATTTTT   1500
GAGACAATAGAAAGCATTCCTCCTCCAAAGGATCCCGAGAAATTCCTCGG
TGACCTCTCCGAAAAGTTGAAAATCCGACGGATAGAGAGACGTATCGCAG   1600
AAATAGATGATATGATAAAGAAAGCTTCAAACGATGAAGAAAGGCGTCTT
CTTCTCTCTATGAAAGTGGATCTCCTCAGAAAAATAAAGAGGAGG        1695
```

FIG. 70

```
MIPREVIEEIKEKVDIVEVISEYVNLTRVGSSYRALCPFHSETNPSFYVH
PGLKIYHCFGCGASGDVIKFLQEMEGISFQEALERLAKRAGIDLSLYRTE    100
GTSEYGKYIRLYEETWKRYVKELEKSKEAKDYLKSRGFSEEDIAKFGFGY
VPKRSSISIEVAEGMNITLEELVRYGIALKKGDRFVDRFEGRIVVPIKND    200
SGHIVAFGGRALGNEEPKYLNSPETRYFSKKKTLFLFDEAKKVAKEVGFF
VITEGYFDALAFRKDGIPTAVAVLGASLSREAILKLSAYSKNVILCFDND    300
KAGFRATLKSLEDLLDYEFNVLVATPSPYKDPDELFQKEGEGSLKKMLKN
SRSFEYFLVTAGEVFFDRNSPAGVRSYLSFLKGWVQKMRRKGYLKHIENL    400
VNEVSSSLQIPENQILNFFESDRSNTMPVHETKSSKVYDEGRGLAYLFLN
YEDLREKILELDLEVLEDKNAREFFKRVSLGEDLNKVIENFPKELKDWIF    500
ETIESIPPPKDPEKFLGDLSEKLKIRRIERRIAEIDDMIKKASNDEERRL
LLSMKVDLLRKIKRR                                        565
```

FIG. 71

```
ATGGCTCTACACCCGGCTCACCCTGGGGCAATAATCGGGCACGAGGCCGT
TCTCGCCCTCCTTCCCCGCCTCACCGCCCAGACCCTGCTCTTCTCCGGCC    100
CCGAGGGGGTGGGGCGGCGCACCGTGGCCCGCTGGTACGCCTGGGGGCTC
AACCGCGGCTTCCCCCCGCCCTCCCTGGGGGAGCACCCGGACGTCCTCGA    200
GGTGGGGCCCAAGGCCCGGGACCTCCGGGGCCGGGCCGAGGTGCGGCTGG
AGGAGGTGGCGCCCCTCTTGGAGTGGTGCTCCAGCCACCCCCGGGAGCGG    300
GTGAAGGTGGCCATCCTGGACTCGGCCCACCTCCTCACCGAGGCCGCCGC
CAACGCCCTCCTCAAGCTCCTGGAGGAGCCCCCTTCCTACGCCCGCATCG    400
TCCTCATCGCCCCAAGCCGCGCCACCCTCCTCCCCACCCTGGCCTCCCGG
GCCACGGAGGTGGCATTCGCCCCCGTGCCCGAGGAGGCCCTGCGCGCCCT    500
CACCCAGGACCCGGAGCTCCTCCGCTACGCCGCCGGGGCCCCGGGCCGCC
TCCTTAGGGCCCTCCAGGACCCGGAGGGGTACCGGGCCCGCATGGCCAGG    600
GCGCAAAGGGTCCTGAAAGCCCCGCCCCTGGAGCGCCTCGCTTTGCTTCG
GGAGCTTTTGGCCGAGGAGGAGGGGGTCCACGCCCTCCACGCCGTCCTAA    700
AGCGCCCGGAGCACCTCCTTGCCCTGGAGCGGGCGCGGGAGGCCCTGGAG
GGGTACGTGAGCCCCGAGCTGGTCCTCGCCCGGCTGGCCTTAGACTTAGA    800
GACA
```

FIG. 72

```
MALHPAHPGAIIGHEAVLALLPRLTAQTLLFSGPEGVGRRTVARWYAWGL
NRGFPPPSLGEHPDVLEVGPKARDLRGRAEVRLEEVAPLLEWCSSHPRER    100
VKVAILDSAHLLTEAAANALLKLLEEPPSYARIVLIAPSRATLLPTLASR
ATEVAFAPVPEEALRALTQDPELLRYAAGAPGRLLRALQDPEGYRARMAR    200
AQRVLKAPPLERLALLRELLAEEEGVHALHAVLKRPEHLLALERAREALE
GYVSPELVLARLALDLET                                     268
```

FIG. 73

```
ATGCTGGACCTGAGGGAGGTGGGGGAGGCGGAGTGGAAGGCCCTAAAGCC
CCTTTTGGAAAGCGTGCCCGAGGGCGTCCCCGTCCTCCTCCTGGACCCTA    100
AGCCAAGCCCCTCCCGGGCGGCCTTCTACCGGAACCGGGAAAGGCGGGAC
TTCCCCACCCCCAAGGGGAAGGACCTGGTGCGGCACCTGGAAAACCGGGC    200
CAAGCGCCTGGGGCTCAGGCTCCCGGGCGGGGTGGCCCAGTACCTGGCCT
CCCTGGAGGGGGACCTCGAGGCCCTGGAGCGGGAGCTGGAGAAGCTTGCC    300
CTCCTCTCCCCACCCCTCACCCTGGAGAAGGTGGAGAAGGTGGTGGCCCT
GAGGCCCCCCCTCACGGGCTTTGACCTGGTGCGCTCCGTCCTGGAGAAGG    400
ACCCCAAGGAGGCCCTCCTGCGCCTAGGCGGCCTCAAGGAGGAGGGGGAG
GAGCCCCTCAGGCTCCTCGGGGCCCTCTCCTGGCAGTTCGCCCTCCTCGC    500
CCGGGCCTTCTTCCTCCTCCGGGAAAACCCCAGGCCCAAGGAGGAGGACC
TCGCCCGCCTCGAGGCCCACCCCTACGCCGCCCGCCGCGCCCTGGAGGCG    600
GCGAAGCGCCTCACGGAAGAGGCCCTCAAGGAGGCCCTGGACGCCCTCAT
GGAGGCGGAAAAGAGGGCCAAGGGGGGGAAAGACCCGTGGCTCGCCCTGG    700
AGGCGGCGGTCCTCCGCCTCGCCCGTTGA
```

FIG. 74

```
MVIAFTGDPFLAREALLEEARLRGLSRFTEPTPEALAQALAPGLFGGGGA
MLDLREVGEAEWKALKPLLESVPEGVPVLLLDPKPSPSRAAFYRNRERRD    100
FPTPKGKDLVRHLENRAKRLGLRLPGGVAQYLASLEGDLEALERELEKLA
LLSPPLTLEKVEKVVALRPPLTGFDLVRSVLEKDPKEALLRLGGLKEEGE    200
EPLRLLGALSWQFALLARAFFLLRENPRPKEEDLARLEAHPYAARRALEA
AKRLTEEALKEALDALMEAEKRAKGGKDPWLALEAAVLRLAR            292
```

FIG. 75

```
ATGGCTCGAGGCCTGAACCGCGTTTTCCTCATCGGCGCCCTCGCCACCCG
GCCGGACATGCGCTACACCCCGGCGGGGCTCGCCATTTTGGACCTGACCC    100
TCGCCGGTCAGGACCTGCTTCTTTCCGATAACGGGGGGGAACCGGAGGTG
TCCTGGTACCACCGGGTGAGGCTCTTAGGCCGCCAGGCGGAGATGTGGGG    200
CGACCTCTTGGACCAAGGGCAGCTCGTCTTCGTGGAGGGCCGCCTGGAGT
ACCGCCAGTGGGAAAGGGAGGGGGAGAAGCGGAGCGAGCTCCAGATCCGG    300
GCCGACTTCCGGACCCCCTGGACGACCGGGGGAAGAAGCGGGCGGAGGAC
AGCCGGGGCCAGCCCAGGCTCCGCGCCGCCCTGAACCAGGTCTTCCTCAT    400
GGGCAACCTGACCCGGGACCCGGAACTCCGCTACACCCCCCAGGGCACCG
CGGTGGCCCGGCTGGGCCTGGCGGTGAACGAGCGCCGCCAGGGGGCGGAG    500
GAGCGCACCCACTTCGTGGAGGTTCAGGCCTGGCGCGACCTGGCGGAGTG
GGCCGCCGAGCTGAGGAAGGGCGACGGCCTTTTCGTGATCGGCAGGTTGG    600
TGAACGACTCCTGGACCAGCTCCAGCGGCGAGCGGCGCTTCCAGACCCGT
GTGGAGGCCCTCAGGCTGGAGCGCCCCACCCGTGGACCTGCCCAGGCCTG    700
CCCAGGCCGGCGGAACAGGTCCCGCGAAGTCCAGACGGGTGGGGTGGACA
TTGACGAAGGCTTGGAAGACTTTCCGCCGGAGGAGGATTTGCCGTTTTGA    800
GCACGAA
```

FIG. 76

```
MARGLNRVFLIGALATRPDMRYTPAGLAILDLTLAGQDLLLSDNGGEPEV
SWYHRVRLLGRQAEMWGDLLDQGQLVFVEGRLEYRQWEREGEKRSELQIR    100
ADFLDPLDDRGKKRAEDSRGQPRLRAALNQVFLMGNLTRDPELRYTPQGT
AVARLGLAVNERRQGAEERTHFVEVQAWRDLAEWAAELRKGDGLFVIGRL    200
VNDSWTSSSGERRFQTRVEALRLERPTRGPAQACPGRRNRSREVQTGGVD
IDEGLEDFPPEEDLPF                                       266
```

FIG. 77

```
AATTCCGACATTTCAATTGAATCGTTTATTCCGCTTGAAAAAGAAGGCAA
GTTGCTCGTTGATGTGAAAAGACCGGGGAGCATCGTACTGCAGGCGCGCT    100
TTTTCTCTGAAATCGTGAAAAAACTGCCGCAACAAACGGTGGAAATCGAA
ACGGAAGACAACTTTTTGACGATCATCCGCTCGGGGCACTCAGAATTCCG    200
CCTCAATGGGCTAAACGCCGACGAATATCCGCGCCTGCCGCAAATTGAAG
AAGAAAACGTGTTTCAAATCCCGGCTGATTTATTGAAAACCGTGATTCGG    300
CAAACGGTGTTCGCCGTTTCTACATCGGAAACGCGCCCAATCTTGACAGG
TGTCAACTGGAAAGTTGAACATGGCGAGCTTGTCTGCACAGCGACCGACA    400
GTCATCGCTTAGCCATGCGCAAAGTGAAAATTGAGTCGGAAAATGAAGTA
TCATACAACGTCGTCATCCCTGGAAAAAGTCTTAATGAGCTCAGCAAAAT    500
TTTGGATGACGGCAACCACCCGGTGGACATCGTCATGACAGCCAATCAAG
TGCTATTTAAGGCCGAGCACCTTCTCTTCTTTTCCCGGCTGCTTGACGGC    600
AACTATCCGGAGACGGCCCGCTTGATTCCAACAGAAAGCAAAACGACCAT
GATCGTCAATGCAAAAGAGTTTCTGCAGGCAATCGACCGAGCGTCCTTGC    700
TTGCTCGAGAAGGAAGGAACAACGTTGTGAAACTGACGACGCTTCCTGGA
GGAATGCTCGAAATTTCTTCGATTTCTCCGAGATCGGGAAAGTGACGGAG    800
CAGCTGCAAACGGAGTCTCTTGAAGGGGAAGAGTTGAACATTTCGTTCAG
CGCGAAATATATGATGGACGCGTTGCGGGCGCTTGATGGAACAGACATTT    900
CAAATCAGCTTCACTGGGGCCATGCGGCCGTTCCTGTTGCGCCCGCTTCA
ACCGATTCGATGCTTCAGCTCATTTTGCCGGTGAGAACATAT            992
```

FIG. 78

```
NSDISIIESFIPLEKEGKLLVDVKRPGSIVLQARFFSEIVKKLPQQTVEI
ETEDNFLTIIRSGHSEFRLNGLNADEYPRLPQIEEENVFQIPADLLKTVI    100
RQTVFAVSTSETRPILTGVNWKVEHGELVCTATDSHRLAMRKVKIIESEN
EVSYNVVIPGKSLNELSKIILDDGNHPVDIVMTANQVLFKAEHLLFFSRL    200
LDGNYPETARLIPTESKTTMIVNAKEFLQAIDRASLLAREGRNNVVKLTT
LPGGMLEISSISPEIGKVTEQLQTESLEGEELNISFSAKYMMDALRALDG    300
TDIQISFTGAMRPFLLRPLHTDSMLQLILPVRTY
```

FIG. 79

```
ATGATTAACCGCGTCATTTTGGTCGGCAGGTTAACGAGAGATCCGGAGTT
GCGTTACACTCCAAGCGGAGTGGCTGTTGCCACGTTTACGCTCGCGGTCA    100
ACCGTCCGTTTACAAATCAGCAGGGCGAGCGGGAAACGGATTTTATTCAA
TGTGTCGTTTGGCGCCGCCAGGCGGAAAACGTCGCCAACTTTTTGAAAAA    200
GGGGAGCTTGGCTGGTGTCGATGGCCGACTGCAAACCCGCAGCTATGAAA
ATCAAGAAGGTCGGCGTGTGTACGTGACGGAAGTGGTGGCTGATAGCGTC    300
CAATTTCTTGAGCCGAAAGGAACGAGCGAGCAGCGAGGGGCGACAGCAGG
CGGCTACTATGGGGATCCATTCCCATTCGGGCAAGATCAGAACCACCAAT    400
ATCCGAACGAAAAAGGGTTTGGCCGCATCGATGACGATCCTTTCGCCAAT
GACGGCCAGCCGATCGATATTTCTGATGATGATTTGCCGTTT            492
```

FIG. 80

```
MINRVILVGRLTRDPELRYTPSGVAVATFTLAVNRPFTNQSYENQEGRRV
YVTEVVADSVQFLEPKGTSEQRGATAGGYYQGERETDFIQCVVWRRQAEN    100
VANFLKKGSLAGVDGRLQTRGDPFPFGQDQNHQYPNEKGFGRIDDDPFAN
DGQPIDISDDDLPF                                        164
```

FIG. 81

```
ATGCTGGAACGCGTATGGGGAAACATTGAAAAACGGCGTTTTTCTCCCCT
TTATTTATTATACGGCAATGAGCCGTTTTTATTAACGGAAACGTATGAGC   100
GATTGGTGAACGCAGCGCTTGGCCCCGAGGAGCGGGAGTGGAACTTGGCT
GTGTACGACTGCGAGGAAACGCCGATCGAGGCGGCGCTTGAGGAGGCCGA   200
GACGGTGCCGTTTTTCGGCGAGCGGCGTGTCATTCTCATCAAGCATCCAT
ATTTTTTTACGTCTGAAAAAGAGAAGGAGATCGAACATGATTTGGCGAAG   300
CTGGAGGCGTACTTGAAGGCGCCGTCGCCGTTTTCGATCGTCGTCTTTTT
CGCGCCGTACGAGAAGCTTGATGAGCGAAAAAAAATTACGAAGCTCGCCA   400
AAGAGCAAAGCGAAGTCGTCATCGCCGCCCCGCTCGCCGAAGCGGAGCTG
CGTGCCTGGGTGCGGCGCCGCATCGAGAGCCAAGGGGCGCAAGCAAGCGA   500
CGAGGCGATTGATGTCCTGTTGCGGCGGGCCGGGACGCAGCTTTCCGCCT
TGGCGAATGAAATCGATAAATTGGCCCTGTTTGCCGGATCGGGCGGAACC   600
ATCGAGGCGGCGGCGGTTGAGCGGCTTGTCGCCCGCACGCCGGAAGAAAA
CGTATTTGTGCTTGTCGAGCAAGTGGCGAAGCGCGACATTCCAGCAGCGT   700
TGCAGACGTTTTATGATCTGCTTGAAAACAATGAAGAGCCGATCAAAATT
TTGGCGTTGCTCGCCGCCCATTTCCGCTTGCTTTCGCAAGTGAAATGGCT   800
TGCCTCCTTAGGCTACGGACAGGCGCAAATTGCTGCGGCGCTCAAGGTGC
ACCCGTTCCGCGTCAAGCTCGCTCTTGCTCAAGCGGCCCGCTTCGCTGAC   900
GGAGAGCTTGCTGAGGCGATCAACGAGCTCGCTGACGCCGATTACGAAGT
GAAAAGCGGGGCGGTCGATCGCCGGTTGGCCGTTGAGCTGCTTCTGATGC  1000
GCTGGGGCGCCCGCCCGGCGCAAGCGGGGCGCCACGGCCGGCGG
```

FIG. 82

```
MLERVWGNIEKRRFSPLYLLYGNEPFLLTETYERLVNAALGPEEREWNLA
VYDCEETPIEAALEEAETVPFFGERRVILIKHPYFFTSEKEKEIEHDLAK   100
LEAYLKAPSPFSIVVFFAPYEKLDERKKITKLAKEQSEVVIAAPLAEAEL
RAWVRRRIESQGAQASDEAIDVLLRRAGTQLSALANEIDKLALFAGSGGT   200
IEAAAVERLVARTPEENVFVLVEQVAKRDIPAALQTFYDLLENNEEPIKI
LALLAAHFRLLSQVKWLASLGYGQAQIAAALKVHPFRVKLALAQAARFAD   300
GELAEAINELADADYEVKSGAVDRRLAVELLLMRWGARPAQAGRHGRR
```

FIG. 83

```
ATGCGATGGGAACAGCTAGCGAAACGCCAGCCGGTGGTGGCGAAAATGCT
GCAAAGCGGCTTGGAAAAAGGGCGGATTTCTCATGCGTACTTGTTTGAGG    100
GGCAGCGGGGGACGGGCAAAAAAGCGGCCAGTTTGTTGTTGGCGAAACGT
TTGTTTTGTCTGTCCCCAATCGGAGTTTCCCCGTGTCTAGAGTGCCGCAA    200
CTGCCGGCGCATCGACTCCGGCAACCACCCTGACGTCCGGGTGATCGGCC
CAGATGGAGGATCAATCAAAAAGGAACAAATCGAATGGCTGCAGCAAGAG    300
TTCTCGAAAACAGCGGTCGAGTCGGATAAAAAAATGTACATCGTTGAGCA
CGCCGATCAAATGACGACAAGCGCTGCCAACAGCCTTCTGAAATTTTTGG    400
AAGAGCCGCATCCGGGGACGGTGGCGGTATTGCTGACTGAGCAATACCAC
CGCCTGCTAGGGACGATCGTTTCCCGCTGTCAAGTGCTTTCGTTCCGGCC    500
GTTGCCGCCGGCAGAGCTCGCCCAGGGACTTGTCGAGGAGCACGTGCCGT
TGCCGTTGGCGCTGTTGGCTGCCCATTTGACAAACAGCTTCGAGGAAGCA    600
CTGGCGCTTGCCAAAGATAGTTGGTTTGCCGAGGCGCGAACATTAGTGCT
ACAATGGTATGAGATGCTGGGCAAGCCGGAGCTGCAGCTTTTGTTTTTCA    700
TCCACGACCGCTTGTTTCCGCATTTTTTGGAAAGCCATCAGCTTGACCTT
GGACTTG                                                757
```

FIG. 84

```
MRWEQLAKRQPVVAKMLQSGLEKGRISHAYLFEGQRGTGKKAASLLLAKR
LFCLSPIGVSPCLECRNCRRIDSGNHPDVRVIGPDGGSIKKEQIEWLQQE    100
FSKTAVESDKKMYIVEHADQMTTSAANSLLKFLEEPHPGTVAVLLTEQYH
RLLGTIVSRCQVLSFRPLPPAELAQGLVEEHVPLPLALLAAHLTNSFEEA    200
LALAKDSWFAEARTLVLQWYEMLGKPELQLLFFIHDRLFPHFLESHQLDL
GL                                                     252
```

FIG. 85

```
GTGGCATACCAAGCGTTATATCGCGTGTTTCGGCCGCAGCGCTTTGCGGA
CATGGTCGGCCAAGAACACGTGACCAAGACGTTGCAAAGCGCCCTGCTTC   100
AACATAAAATATCGCACGCTTACTTATTTTCCGGCCCGCGCGGTACAGGA
AAAACGAGCGCAGCGAAAATTTTCGCCAAGGCGGTCAACTGTGAACAGGC   200
GCCAGCGGCGGAGCCATGCAATGAGTGTCCAGCTTGCCTCGGCATTACGA
ATGGAACGGTTCCCGATGTGCTGGAAATTGACGCTGCTTCCAACAACCGC   300
GTCGATGAAATTCGTGATATCCGTGAGAAGGTGAAATTTGCGCCAACGTC
GGCCCGCTACAAAGTGTATATCATCGACGAGGTGCATATGCTGTCGATCG   400
GTGCGTTTAACGCGCTGTTGAAAACGTTGGAGGAGCCGCCGAAACACGTC
ATTTTCATTTTGGCCACGACCGAGCCGCACAAAATTCCGGCGACGATCAT   500
TTCCCGCTGCCAACGGTTCGATTTTCGCCGCATCCCGCTTCAGGCGATCG
TTTCACGGCTAAAGTACGTCGCAAGCGCCCAAGGTGTCGAGGCGTCAGAT   600
GAGGCATTGTCCGCCATCGCCCGTGCTGCAGACGGGGGGATGCGCGATGC
GCTCAGCTTGCTTGATCAAGCCATTTCGTTCAGCGACGGGAAACTTCGGC   700
TCGACGACGTGCTGGCGATGACCGGGGCTGCATCATTTGCCGCCTTATCG
AGCTTCATCGAAGCCATCCACCGCAAAGATACAGCGGCGGTTCTTCAGCA   800
CTTGGAAACGATGATGGCGCAAGGGAAAGATCCGCATCGTTTGGTTGAAG
ACTTGATTTTGTACTATCGCGATTTATTGCTGTACAAAACCGCTCCCTAT   900
GTGGAGGGAGCGATTCAAATTGCTGTCGTTGACGAAGCGTTCACTTCACT
GTCGGAAATGATTCCGGTTTCCAATTTATACGAGGCCATCGAGTTGCTGA  1000
ACAAAAGCCAGCAAGAGATGAAGTGGACAAACCACCCGCGCCTTCTGTTG
GAAGTGGCGCTTGTGAAACTTTGCCATCCATCAGCCGCCGCCCCGTCGCT  1100
GTCGGCTTCCGAGTTGGAACCGTTGATAAAGCGGATTGAAACGCTGGAGG
CGGAATTGCGGCGCCTGAAGGAACAACCGCCTGCCCCTCCGTCGACCGCC  1200
GCGCCGGTGAAAAAACTGTCCAAACCGATGAAAACGGGGGGGATATAAAGC
CCCGGTTGGCCGCATTTACGAGCTGTTGAAACAGGCGACGCATGAAGATT  1300
TAGCTTTGGTGAAAGGATGCTGGGCGGATGTGCTCGACACGTTGAAACGG
CAGCATAAAGTGTCGCACGCTGCCTTGCTGCAAGAGAGCGAGCCGGTTGC  1400
AGCGAGCGCCTCAGCGTTTGTATTAAAATTCAAATACGAAATCCACTGCA
AAATGGCGACCGATCCCACAAGTTCGGTCAAAGAAAACGTCGAAGCGATT  1500
TTGTTTGAGCTGACAAACCGCCGCTTTGAAATGGTAGCCATTCCGGAGGG
AGAATGGGGAAAAATAAGAGAAGAGTTCATCCGCAATAAGGACGCCATGG  1600
TGGAAAAAAGCGAAGAAGATCCGTTAATCGCCGAAGCGAAGCGGCTGTTT
GGCGAAGAGCTGATCGAAATTAAAGAA                          1677
```

FIG. 86

```
VAYQALYRVFRPQRFADMVGQEHVTKTLQSALLQHKISHAYLFSGPRGTG
KTSAAKIFAKAVNCEQAPAAEPCNECPACLGITNGTVPDVLEIDAASNNR   100
VDEIRDIREKVKFAPTSARYKVYIIDEVHMLSIGAFNALLKTLEEPPKHV
IFILATTEPHKIPATIISRCQRFDFRRIPLQAIVSRLKYVASAQGVEASD   200
EALSAIARAADGGMRDALSLLDQAISFSDGKLRLDDVLAMTGAASFAALS
SFIEAIHRKDTAAVLQHLETMMAQGKDPHRLVEDLILYYRDLLLYKTAPY   300
VEGAIQIAVVDEAFTSLSEMIPVSNLYEAIELLNKSQQEMKWTNHPRLLL
EVALVKLCHPSAAAPSLSASELEPLIKRIETLEAELRRLKEQPPAPPSTA   400
APVKKLSKPMKTGGYKAPVGRIYELLKQATHEDLALVKGCWADVLDTLKR
QHKVSHAALLQESEPVAASASAFVLKFKYEIHCKMATDPTSSVKENVEAI   500
LFELTNRRFEMVAIPEGEWGKIREEFIRNKDAMVEKSEEDPLIAEAKRLF
GEELIEIKE                                             559
```

FIG. 87

```
ATGGTGACAAAAGAGCAAAAAGAGCGGTTTCTCATCCTGCTTGAGCAGCT
GAAGATGACGTCGGACGAATGGATGCCGCATTTTCGTGAGGCAGCCATTC    100
GCAAAGTCGTGATCGATAAAGAGGAGAAAAGCTGGCATTTTTATTTTCAG
TTCGACAACGTGCTGCCGGTTCATGTATACAAAACGTTTGCCGATCGGCT    200
GCAGACGGCGTTCCGCCATATCGCCGCCGTCCGCCATACGATGGAGGTCG
AAGCGCCGCGCGTAACTGAGGCGGATGTGCAGGCGTATTGGCCGCTTTGC    300
CTTGCCGAGCTGCAAGAAGGCATGTCGCCGCTTGTCGATTGGCTCAGCCG
GCAGACGCCTGAGCTGAAAGGAAACAAGCTGCTTGTCGTTGCCCGCCATG    400
AAGCGGAAGCGCTGGCGATCAAACGGCGGTTCGCCAAAAAAATCGCTGAT
GTGTACGCTTCGTTTGGGTTTCCCCCCCTTCAGCTTGACGTCAGCGTCGA    500
GCCGTCCAAGCAAGAAATGGAACAGTTTTTGGCGCAAAAACAGCAAGAGG
ACGAAGAGCGAGCGCTTGCTGTACTGACCGATTTAGCGAGGGAAGAAGAA    600
AAGGCCGCGTCTGCGCCGCCGTCCGGTCCGCTTGTCATCGGCTATCCGAT
CCGCGACGAGGAGCCGGTGCGGCGGCTTGAAACGATCGTCGAAGAAGAGC    700
GGCGCGTCGTTGTGCAAGGCTATGTATTTGACGCCGAAGTGAGCGAATTA
AAAAGCGGCCGCACGCTGTTGACCATGAAAATCACAGATTACACGAACTC    800
GATTTTAGTCAAAATGTTCTCGCGCGACAAAGAGGACGCCGAGCTTATGA
GCGGCGTCAAAAAAGGCATGTGGGTGAAAGTGCGCGGCAGCGTGCAAAAC    900
GATACGTTCGTCCGTGATTTGGTCATCATCGCCAACGATTTGAACGAAAT
CGCCGCAAACGAACGGCAAGATACGGCGCCGGAAGGGGAAAAGAGGGTCG   1000
AGCTCCATTTGCATACCCCGATGAGCCAAATGGACGCGGTCACCTCGGTG
ACAAAACTCATTGAGCAAGCGAAAAAATGGGGGCATCCGGCGATCGCCGT   1100
CACCGACCATGCCGTTGTTCAGTCGTTTCCGGAGGCCTACAGCGCGGCGA
AAAAACACGGCATGAAGGTCATTTACGGCCTTGAGGCGAACATCGTCGAC   1200
GATGGCGTGCCGATCGCCTACAATGAGACGCACCGCCGTCTTTCGGAGGA
AACGTACGTCGTCTTTGACGTCGAGACGACGGGCCTGTCGGCTGTGTACA   1300
ATACGATCATTGAGCTGGCGGCGGTGAAAGTGAAAGACGGCGAGATCATC
GACCGATTCATGTCGTTTGCCAACCCTGGACATCCGTTGTCGGTGACAAC   1400
GATGGAGCTGACTGGGATCACCGATGAGATGGTGAAAGACGCCCCGAAGC
CGGACGAGGTGCTAGCCCGTTTTGTTGACTGGGCCGGCGATGCGACGCTT   1500
GTTGCCCACAACGCCAGCTTTGACATCGGTTTTTTAAACGCGGGCCTCGC
TCGCATGGGGCGCGGCAAAATCGCGAATCCAGTCATCGATACGCTCGAGC   1600
TGGCCCGTTTTTTATACCCGGATTTGAAAAACCATCGGCTCAATACATTG
TGCAAAAAATTTGACATTGAATTGACGCAGCATCACCGCGCCATCTACGA   1700
CGCGGAGGCGACCGGGCATTTGCTTATGCGGCTGTTGAAGGAAGCGGAAG
AGCGCGGCATACTGTTTCATGACGAATTAAACAGCCGCACGCACAGCGAA   1800
GCGTCCTATCGGCTTGCGCGCCCGTTCCATGTGACGCTGTTGGCGCAAAA
CGAGACTGGATTGAAAAATTTGTTCAAGCTTGTGTCATTGTCGCACATTC   1900
AATATTTTCACCGTGTGCCGCGCATCCCGCGCTCCGTGCTCGTCAAGCAC
CGCGACGGCCTGCTTGTCGGCTCGGGCTGCGACAAAGGAGAGCTGTTTGA   2000
CAACTTGATCCAAAAGGCGCCGGAAGAAGTCGAAGACATCGCCCGTTTTT
ACGATTTTCTTGAAGTGCATCCGCCGGACGTGTACAAGCCGCTCATCGAG   2100
ATGGATTATGTGAAAGACGAAGAGATGATCAAAAACATCATCCGCAGCAT
CGTCGCCCTTGGTGAGAAGCTTGACATCCCGGTTGTCGCCACTGGCAACG   2200
```

FIG. 88A

TCCATTACTTGAACCCAGAAGATAAAATTTACCGGAAAATCTTAATCCAT
TCGCAAGGCGGGGCGAATCCGCTCAACCGCCATGAACTGCCGGATGTATA 2300
TTTCCGTACGACGAATGAAATGCTTGACTGCTTCTCGTTTTTAGGGCCGG
AAAAAGCGAAGGAAATCGTCGTTGACAACACGCAAAAAATCGCTTCGTTA 2400
ATCGGCGATGTCAAGCCGATCAAAGATGAGCTGTATACGCCGCGCATTGA
AGGGGCGGACGAGGAAATCAGGGAAATGAGCTACCGGCGGGCGAAGGAAA 2500
TTTACGGCGACCCGTTGCCGAAACTTGTTGAAGAGCGGCTTGAGAAGGAG
CTAAAAAGCATCATCGGCCATGGCTTTGCCGTCATTTATTTGATCTCGCA 2600
CAAGCTTGTGAAAAAATCGCTCGATGACGGCTACCTTGTCGGGTCGCGCG
GATCGGTCGGCTCGTCGTTTGTCGCGACGATGACGGAAATCACCGAGGTC 2700
AATCCGCTGCCGCCGCATTACGTTTGCCCGAACTGCAAGCATTCGGAGTT
CTTTAACGACGGTTCAGTCGGCTCAGGGTTTGATTTGCCGGATAAAAACT 2800
GCCCGCGATGTGGGACGAAATACAAGAAAGACGGGCACGACATCCCGTTT
GAGACGTTTCTCGGCTTTAAAGGCGACAAAGTGCCGGATATCGACTTGAA 2900
CTTTTCCGGCGAATACCAGCCGCGCGCCCACAACTATACGAAAGTGCTGT
TTGGCGAAGACAACGTCTACCGCGCCGGGACGATTGGCACGGTCGCTGAC 3000
AAAACGGCGTACGGATTTGTCAAAGCGTATGCGAGCGACCATAACTTAGA
GCTGCGCGGCGCGGAAATCGACGGCTCGCGGCTGGCTGCACCGGGGTGAA 3100
GCGGACGACCGGGCAGCATCCGGGCGGCATCATCGTCGTCCCGGATTATA
TGGAAATTTACGATTTTACGCCGATTCAATATCCGGCCGATGACACGTCC 3200
TCTGAATGGCGGACGACCCATTTCGACTTCCATTCGATCCACGACAATTT
GTTGAAGCTCGATATTCTCGGGCACGACGATCCGACGGTCATTCGCATGC 3300
TGCAAGATTTAAGCGGCATCGATCCGAAAACGATCCCGACCGACGACCCG
GATGTGATGGGCATTTTCAGCAGCACCGAGCCGCTTGGCGTTACGCCGGA 3400
GCAAATCATGTGCAATGTCGGCACGATCGGCATTCCGGAGTTTGGCACGC
GCTTCGTTCGGCAAATGTTGGAAGAGACAAGGCCAAAAACGTTTTCCGAA 3500
CTCGTGCAAATTTCCGGCTTGTCGCACGGCACCGATGTGTGGCTCGGCAA
CGCGCAAGAGCTCATTCAAAACGGCACGTGTACGTTATCGGAAGTCATCG 3600
GCTGCCGCGACGACATTATGGTCTATTTGATTTACCGCGGGCTCGAGCCG
TCGCTCGCTTTTAAAATCATGGAATCCGTGCGCAAAGGAAAAGGCTTAAC 3700
GCCGGAGTTTGAAGCAGAAATGCGCAAACATGACGTGCCGGAGTGGTACA
TCGATTCATGCAAAAAAATCAAGTACATGTTCCCGAAAGCGCACGCCGCC 3800
GCCTACGTGTTAATGGCGGTGCGCATCGCCTACTTTAAGGTGCACCATCC
GCTTTTGTATTACGCGTCGTACTTTACGGTGCGGGCGGAGGACTTTGACC 3900
TTGACGCCATGATCAAAGGATCACCCGCCATTCGCAAGCGGATTGAGGAA
ATCAACGCCAAAGGCATTCAGGCGACGGCGAAAGAAAAAAGCTTGCTCAC 4000
GGTTCTTGAGGTGGCCTTAGAGATGTGCGAGCGCGGCTTTTCCTTTAAAA
ATATCGATTTGTACCGCTCGCAGGCGACGGAATTCGTCATTGACGGCAAT 4100
TCTCTCATTCCGCCGTTCAACGCCATTCCGGGGCTTGGGACGAACGTGGC
GCAGGCGATCGTGCGCGCCCGCGAGGAAGGCGAGTTTTTGTCGAAGGAGG 4200
ATTTGCAACAGCGCGGCAAATTGTCGAAAACGCTGCTCGAGTATCTAGAA
AGCCGCGGCTGCCTTGACTCGCTTCCAGACCATAACCAGCTGTCGCTGTT 4300
T

FIG. 88B

MVTKEQKERFLILLEQLKMTSDEWMPHFREAAIRKVVIDKEEKSWHFYFQ
FDNVLPVHVYKTFADRLQTAFRHIAAVRHTMEVEAPRVTEADVQAYWPLC 100
LAELQEGMSPLVDWLSRQTPELKGNKLLVVARHEAEALAIKRRFAKKIAD
VYASFGFPPLQLDVSVEPSKQEMEQFLAQKQQEDEERALAVLTDLAREEE 200
KAASAPPSGPLVIGYPIRDEEPVRRLETIVEEERRVVVQGYVFDAEVSEL
KSGRTLLTMKITDYTNSILVKMFSRDKEDAELMSGVKKGMWVKVRGSVQN 300
DTFVRDLVIIANDLNEIAANERQDTAPEGEKRVELHLHTPMSQMDAVTSV
TKLIEQAKKWGHPAIAVTDHAVVQSFPEAYSAAKKHGMKVIYGLEANIVD 400
DGVPIAYNETHRRLSEETYVVFDVETTGLSAVYNTIIELAAVKVKDGEII
DRFMSFANPGHPLSVTTMELTGITDEMVKDAPKPDEVLARFVDWAGDATL 500
VAHNASFDIGFLNAGLARMGRGKIANPVIDTLELARFLYPDLKNHRLNTL
CKKFDIELTQHHRAIYDAEATGHLLMRLLKEAEERGILFHDELNSRTHSE 600
ASYRLARPFHVTLLAQNETGLKNLFKLVSLSHIQYFHRVPRIPRSVLVKH
RDGLLVGSGCDKGELFDNLIQKAPEEVEDIARFYDFLEVHPPDVYKPLIE 700
MDYVKDEEMIKNIIRSIVALGEKLDIPVVATGNVHYLNPEDKIYRKILIH
SQGGANPLNRHELPDVYFRTTNEMLDCFSFLGPEKAKEIVVDNTQKIASL 800
IGDVKPIKDELYTPRIEGADEEIREMSYRRAKEIYGDPLPKLVEERLEKE
LKSIIGHGFAVIYLISHKLVKKSLDDGYLVGSRGSVGSSFVATMTEITEV 900
NPLPPHYVCPNCKHSEFFNDGSVGSGFDLPDKNCPRCGTKYKKDGHDIPF
ETFLGFKGDKVPDIDLNFSGEYQPRAHNYTKVLFGEDNVYRAGTIGTVAD 1000
KTAYGFVKAYASDHNLELRGAEIDLAAGCTGVKRTTGQHPGGIIVVPDYM
EIYDFTPIQYPADDTSSEWRTTHFDFHSIHDNLLKLDILGHDDPTVIRML 1100
QDLSGIDPKTIPTDDPDVMGIFSSTEPLGVTPEQIMCNVGTIGIPEFGTR
FVRQMLEETRPKTFSELVQISGLSHGTDVWLGNAQELIQNGTCTLSEVIG 1200
CRDDIMVYLIYRGLEPSLAFKIMESVRKGKGLTPEFEAEMRKHDVPEWYI
DSCKKIKYMFPKAHAAAYVLMAVRIAYFKVHHPLLYYASYFTVRAEDFDL 1300
DAMIKGSPAIRKRIEEINAKGIQATAKEKSLLTVLEVALEMCERGFSFKN
IDLYRSQATEFVIDGNSLIPPFNAIPGLGTNVAQAIVRAREEGEFLSKED 1400
LQQRGKLSKTLLEYLESRGCLDSLPDHNQLSLF

FIG. 89